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Copyright (a) 1991 - 2003 Compages Lid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D; Indels C; Gaps
                                                                                                                                                                                                                                                                                                                           Mature HSA-A may be produced using the sequence incorporated into a plasmid vector with suitable controllers, and transfered to a yeast expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Oucry March (0) 14: Score 3.63; EB 11; Length 585; EB 4 configurating 166,14; Pref. No. 9, 55-252 Marches 95; Conservative 6; Mismarches 9; Indels 9;
                                                                                                                                                                                                     Human secun alburin press. ny yeast host.
by oithining transformed plasmid yeast to produce serum, and
viviling 11.
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                                                                             26-00T 1958; 86JP 0258302.
                                                                                                                CTOFUL - TOA NEBRYO KODYO KK
                                      8877-3268302
                                                                                                                                                    NPT. 1990-176228/21.
N-FSDB, AAQ04719.
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71-YOF-1330
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Fleet Local Sinilarity 100.01; Pred No. 9.5e-255; Date 1 Gaps
Hatches 565; Conservative C, Misnatches O; Indels 3; Gaps
                                                                          Wature process of tunan serum albuman tree corresp. AANOGES. Used to make new Viterennal tragments which are used as plasma expanders, or as sucstitutes to: HisA or HSA, in tissue militaredla. (Spaked on 25-MAR-200) to correct PA field.)

    esp. useful as blood plasma expanders

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                                      Disclosure, fig 2, 20pp. English
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361 GAAADHEGAAXPEFKEUNEEPONLIKONCELFROLGEYKROKALLURYTKKUPCYST 420
361 GAAADHEGAAXPEFKEUNEEPONLIKONCELFROLGEYKROKALLURYTKKUPCYST 420
                                  CLPSLAADFVESKUVCKTYAEAKDVELGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKC 360
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          DIFSLAADFVESKUVCKNYAEAKDVFLGMFLYEYARRHPDYSVVILIRLAKTYETTLEKC 160
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artivity - used to societe human albumin without prodm. of the 45
X2 trapts.
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Sacobaronyo, B cerevisiao,
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17-JAN-1996 (first entry)
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N-PSDB: AAC99695.
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24: WFIECHDILLIAMYLLENDSISSKLÄSCCERPLEKSHCIAEVENEEMA 303
24: WFIECHDILEADARDIAMYLCENDSISSKLÄSCERPLEKSHCIAEVENEEMA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fragments A-C of HSA are expressed as fusion proteins with the signal peptide of E coll salvaline prosphatase. The fragments are selected for their specific properties. The Creeninal francaed fragment. B. does not bind long-chain fatry acids but does not bind long-chain fatry acids but does not bind long-chain fatry acids but forebut to various redicines at the central legion. The N-terminal truncated fragment. C. has good stability in protein folding. The central segment. A. has characteristics of both B and C. See also AACC596-096-098.

(Updated on 25-AAR-2001 to cornect PC field.)
(Updated on 25-AAR-2001 to cornect PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human serum albumin fragments - used to bond medicines and for stable folding of protein(s).
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Scott 1031, DB 11, Length 955, Beet Local Shrilwity 10.0%, Pred. No.958-255, Softwative 0, Misharches 1, Indels 0; Maches 551, Conservative 0, Misharches 1, Indels 0;
                                                                                                                                                                             Location/Qualifiers
123.303
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                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1985; 89JP-0217540
                                                                                                                                                                                                                                                                                                                                                                                                                                                        89JF-0217540
                                                                                                                                                                                                                                         1..303
/label= B
121..585
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25-MAR-2003 (updated)
16-APR-1991 (first entry)
                                                         Human serum albumin
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N-PSDB; AAQ36099.
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                                                                                                 HSA: folding: ss
                                                                                                                                                                                                                                                                                                                                       JP62227C79-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-AUG-1989;
                                                                                                                                          Homo sapiens
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61 RODECHELRORELDYATLRETYGENACCAKCEFERRECFUCHKODYANLARLYPPEV 120
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241 VITECERDLEGALDEATHALIAKYTCERCUSTSKILKECERFILEKSHGTAEVENDERA JUD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DAHKSEVAHREKDLGEENEKALVIIAFAQYIQQCPFEDHYKLYNEVTEFAKTOVADESAE 60
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                                                                                                      the invention relates to a serum alturant-growth hormone fusion protein useful to freed growth hormone related discosses such as Down's syndione. This sequence represents a 45A protein related to the serum albumingrowth hormone protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hurdu: alburin; ischanic state; serum procenn; motal ion sait;
perioperativo ischanica; kschemia; myccardial infarction;
progressivo curbiary arreny disease.
                                                                                                                                                                                                                                                                                                                                                                                              Opery Mich 10.1A: Score 3.103; IB 18: Length 585; Sect Local Sinilarity 100.1A; Pred. No. 9.5e-258. Makether 84: Mishatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amine acid sequence of a human albumin protein.
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                                     Disclosure: Fig 6: 21pp; Korean.
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                                                                                                                                                                                                                                                                                                                   Sequence 585 AA;
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121 DYMCTAHDONESTEKKYLNEIARHYYFARBLUFRAKYKAFTECGAASTAACHE 189
121 DYMCTAHDONESTEKKYLNEIARHYYFARBLUFRAKYKAFTECGAASTAGAAFTECGAASTAACHE 189
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                                                                                                                                                                                                  61 MODKSCHTLEGDKLGTVATCRETYGEMADGGAKGSFERNEGFLCHKDONPNLPRCVRPRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHTBCCHGDLLECADGRACLAKYICENQDSISSKIKBCCHKFLLEKSHCIASVENDENG 300
                                DAHKSEVAHREKOLGEENEKALVIJAFAQYIQOORPEDHUKLVMEVTERAKTOVAOESAE 60
                                                                                Serum alburin-growth hormone fusion protein - useful to treat growth hormone related diseases, e.g. Down's syndrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serum albumin-growth hormone fusion protein, growth hormone.
Down's syndrome.
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N-PSDB, AAK99568.
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19-DEC-1996;
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41. PILVENGANIGACOSKONDRAKRAPOKABULANVANOGOGIAHKTPVABAVIKOGTES 480
                                                                                                                                                                      48: INNERPOPSALEVORTVYFRERNAETFTRABICTISEKERQIKKQTADVELVEKKAT 540
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                                                                                       (2) PTIVEVSRKISKVGSKCOMPRBAKRAPONEDYLSVVINQLOVLHEKTFVSDRVIKOCTES 480
                                                                                                                                      481 CUNRESCESALEVEETYVPKEENAETETERADICTISEKERQIRKÇTALVELVKHKPKAT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The method relates to a method of recombinantly producing human serum albumin (HGM) in year by altering the coding sequence of 18.4 to comperted as these codon has the compete HSA gene (NAA1003); was generated as three synthesis in tagments (AAA1003-A1004); was generated as three synthesis of HSA fargetts (AAA1003-A1004); coned by recombinant that rechology, Each HSA fargetts was synthesised from overleption to the representation of the HSA encoded by the human gene with a yeast codon bias. The invention also covers a recombinant generated from the process for producing carrying the recombinant expression which is process for producing the recombinant expression where the process for producing human serum albumin in the yeast hose codes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Process for preparing recombined human serum albunin - which comprises yeast biased sex codons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant, human setur albumin, ESA) yeast modon bias, nost cell
overlapping oligonucleotide, expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast codon-brased recombinant human serum albumin protein.
                                                                                                                                                                                                                                 541 RECHANDOPARVEXCORADOXEDCEAESCRICUS 585
                                                                                                                                                                                                                                                             (HALU-) HALLI BIOENGINEERING CO LTD
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N-FSDB; AAA10091.
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Synthetic.
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331 DIPELAADTYESKOTCKYARAKOVEGHIJETAREPOTSVYJLIELAKTYETTIJEC 360
331 DIPELAADTYESKOTCKYARAKOVEGHIJETAREPOTSVYJLIALAKTYETTIJEC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            New method for the continuous detection of isohemic states comprises detecting and quantifying the existence of an alteration of the serum protein albumin -
/note= "optionally acetylated, and claimed under
claim 56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 97-106; 105pp; English
                                                                                                                                                                                                                                                                                                                               (ISCH-) ISCHEMIA TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                              Bar-Or D, Sau E, Winkler JV,
                                                                                                                                                                                                        98US-0162939,
98US-016581,
98US-0165926,
99US-0115392,
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62-0CT-1998,
62-0CT-1998,
11-0AM-1999,
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The present invention describes an albumin fusion protein (1) comprising a time protein. Yau'd (a fragement extrained (3) albumin (2) comprising a time (2) protein. Yau'd (a fragement extrained (3) albumin (2) comprising a time (2) y defined sequence in ABS70006 of 685 amno actions. Where the fragment or variant has albumin or therepetic protein X activities. Albumin (1910) proteins are stablished in muncosuppressive.

Antidadelic. International constitution and poortalic activities. Albumin (1910) proteins are stablished therefore in C3. C34 and C36 useful for treating various diseases antidadelic C3. C34 and C36 useful for treating various diseases. C3 antidadelic C3 and C30 useful for treating various diseases antidadelic C3. C34 and C36 useful for treating various diseases antidadelic proteins. Fining albumin to therapeutic proteins stablishes the citerature protein activity it also reduces the need to formulate the protein solutions with large excesses of carrier proteins astallishes the constant solutions with large excesses of carrier proteins and expense of carrier proteins and equipment of the finite of the fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New alburin fusion proteins, useful for treating diseases and disorders such as cancer, comprise therapeutic protein fused to albumin
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278.252
278.257
770.6 "H) extible unter-subdomain linker region"
7.267.2 Subdomain
2.6.781
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3.6.7.29
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10.04: Secret 3063, DB 22; Length SB: 
Medicard Scotty 10.0 No Peed, No. 3, Sec. 25.
Medicard SB: Conservative 3, Mismatches 6: Indels 9, Mascher SB: Conservative 9.
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3.92. 4.10
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25-APR 2000/ 20008-199364P.
21-ESC-2000/ 20008-256931P.
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241 VHTECCHODILECATORNALARYICENOPSISEKIAKTOCRRPILEKSHÇIAKUFEN DO.
241 VHTECCHODILECATORNALARYICENOPSISEKIAKTOKRPILEKSHÇIAKUFEN DO.
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421 ITLOBYDSKI GKYSKYCKABRÁKARMCAEDYLSVLAGCCVLHRYTVSCHYTKYTTER 450
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    61 NOMESTATIFGUKACTVATURETYGEKADCOANGEPERRICFLCHKODNENTALTREEV 120
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421 PTLYEVSRILGKVGSKCCHPBAARHCARDYJSVYLNGLCVLHEKTRYSDRVTKCTD3 483
421 PTLYEVSRILGKVGSKCCHPBAARHCARDYJSVYLNGLCVLHEKTRYSDRVTKCTD3 483
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Huran, albumin, HA, fusion protein; inmune system disorder, syphilis, transplant rejections; blood related disorder, mydocardia, infastion: hypespoilifecture disorder, active mysion (cukkemia: renal disorder, glometrionephilis), cardiovascular disorder, arthythmia, rhimin, regimetriaring disorder, neurologica, disorder, arthythmia, rhimin, regimetriaring disorder, neurologica, disorse, arthythmia, rhimin, remembers, phecycochicona, reproductive system disorder, messes, gastronicestual disorder, included the system disorder, melanoma, gene thorapy virus, wound hoaling, renal coll carcinoma,
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The present invention selates to albumin fusion processe, which corprise a tichogening process and diburin. The present sequence is the protesm of expense of the process sequence is the protesm of the present invention. The albumin fisher process of the first process of the present invention. The albumin fisher process are discipled as the reastern prevention disappass, and/or decent on of discipled as the present invention. The albumin fisher process of discipled as the prevention of the reastern prevent prevention discipled as the prevention of the present as the prevention of th
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18. KLDELKESAKSAKKIKKASICKFTERAFKANAVASUSPEYAESAKSUVTULIK 240
18. KLDELKESAKSAKKIKKASICKFTERAFKANAVASUSPEYAERRUSKUVTULIK 240
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wan, albumin, HA; fusion protein, therapeutic protein, valuerary, use agget disorder, transpan respector) back sealed alsorder. Iteratal interaction by protein and disorder, allower increping a little acceleration of society and experience of experience Location/Qualifiers 54..61 /label* loop.1 76..89 362.368 /labeix Loop_VIII 439.447 /labeix Loop_IX 461.475 /labeix Loop_X / Abbel 100p 11 92.100 12.250 17.252 17.252 12.252 475, 495 /label= Leop_XI 560..564 /label= Leop_XII LCop X da-) HUMAN GENOME SCI INC APR-2000; 2000US-229358F. APR-2000: 2000US-199384F. DEC-2000; 2000US-256931P APR-2001: 2001WO-US:1924 CA, Haseltine WA; 2001-616754/71. DB; AAD21538. 33179443-82 CT - 2001. 2 11.2 37.0 2.3 rin ניננ 1.7 9 1 1.5

unin fusion proteins computating a therapeutic protein and albunin, in a file treating lumine system disorders (e.g., transplant coins), blood related disorders (e.g., myocardial infarction) and arpoliterative disorders.

Claim 1, Fig 9; 380pp; English.

The invention relates to albumin fusion proteins contrising therapeutic protein fused to a hour, have an extended shelf-like. The albumin tusion proteins are useful in the treatment, prevention, dispanses and/or detection of diseases, disorders such as intuine system disorders le.g. transplant refection? Disod respections of disorders con a intuine system disorders le.g. transplant refection; bytemptodiscipling disorders le.g. controllers in the section; controllers in the disorders le.g. stringthings;

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541 KECLKAMIDERAPURKCZKADKETCRRECKKLVARGAALGL 593 AAB12403 standard: Protein: 585 18 DEC-2001 (first entry) 585 A. Human albumin (HA) Sequence 3÷1 AAE12403: AAE 2401 III AAE 2 82888888 8 8 ô 盘 ć 9 8 8 8 A 3 8 3 8 8 8 ô 8 8 8

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Best Liccal Similarity 100.0%; Secre 310.5; DH 22, Length 535;
Best Liccal Similarity 100.0%; Pred, No. 9.56-255.

Marches 555, Conservative 0; Mismatches 0; Indels 0;
Marches 555, Conservative 0; Mismatches 0; Indels 0; 141 RECLANMEDPARFUENCOMADDMETCEREBONKLVAASCALGL 585 AAE08278 standard, Protein, 585 9603-0769746 9603-0769746 19-MOV-2001 [first entry] Human serum albumin (HSA). Sonnenschein C. Scto AM, STRUE VINI (TEUT) 19-DEC-1996; 19-DEC-1996; US6274305-B1. Home saplens 14-AUG-2001 ASEDESTR. A. A. Son in Son 윤 કે S 8 Š 8 8 8 g 8 8

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                                                                                                                                                                                                                                                                                                                              The invention related to a rethod for insting cancer cells. The nethod is described to reasoning them cancer cell problemation between the results problematic or abbunity the potential for inhititing cancer cells problematic using abbunin derived peptides. The invention is also useful for days survening assays, as a set, as for evaluating capside function the present degrees of survening is busen securial bound (RRA) intaced to the invention.
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                                                                                                                   Medsuring human cell proliferation, useful in drug screening to
decremine the potential for inhibiting cancer cell proliferation and
for evaluating biogeted tumors, comprises employing albumin-derived
poptide.
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Best Local Similarity (CO.Ch. Fred. No. 9,55-25; Length 36%,
Best Local Similarity (CO.Ch. Pred. No. 9,55-252)

Matches 95; Conservative () Mismarches 3; Indels 3,

Matches 95; Conservative () Mismarches 3; Indels 3,
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New fusion protein for treating disease e.g. diabetes comprises an albunin fused to a therapeutic protein \dot{\gamma}
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10. Ch. Score 1303, DB 23, Dength 595;

Best Local Similarity 100,00, Pred No -56-258,

Machee 555, Christivalive C. Mishalches D. Indels C.
                                                                                                            ARG63321 standard; protein; 585 AA
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3103
1 DAHKSEVAHRRKOLGBENFK......TOFNSEGKLVAASOAALGL
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2: /cgn2_6/prodats_A//inan/SA.CMB.pep.*
3: /cgn2_6/prodats_A//inan/SA.CMB.pep.*
4: /cgn2_6/prodats_A//inan/SA.CMB.pep.*
5: /cgn2_6/prodats_A/2inan/SA.CMB.pep.*
6: /cgn2_6/prodats_A/2inan/SACMS.CMB.pep.*
                           GenCore warsion 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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No.
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14 Application (1988) (SECURIOR CHARACTERISTICS: LEWITH: 585 aring acid TYPE: aming acid
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61 NOBKSLHTLFGDRUGGVATLRETYGBRADGCARGBFBRNBGFJGHKDDNPNLPRLVPEV 120
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121 DYNCTAFEDHETFEKKLYKTAKARPTYAFELFFANKYKAAFTECCCAASKACLEF 190
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                                                                                                          CONTRACTOR TO THE CONTRACT OF 
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10.31; Score 3103; DB 1; Jength 585;
Al Similarity 10.08; Pred. No. 9, 9.42-25; Indels C: Sapo
895; Conservative C: Mismatches C: Indels C: Sapo
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LOCATION: 189 449 0
OTHER INFORMATION: /Antes "Alternative Clermin; of
OTHER INFORMATION: H5A'i.n)"
NAME/KEY
CTHER INFORMATION: /Amino acid sequence of
US-28-153-799-14
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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ORGANISH: HOTO SAPIHUS
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Best Local Si
Matches 585)
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TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SOUGHNESS: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Center, Patent Operations/RRC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATA APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJORESSES: Amgen Center, Patent Operations/RRC STREET: 1840 DeHavilland Drive Thousand Oaks STATE: California
                                                          ز:
                    Score 3099; DB 4;
Pred. No. 2.4e-286;
1; Mismatches 0;
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CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
                    99.9%;
                  Query Match
Best Local Similarity 99.8
Matches 584; Conservative
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                                                                                                                             Score 3099; DB 1;
Pred. No. 2.4e-296;
0; Mismatches 1;
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Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fuelon Polypeptides
FILE REPERENCE: 60-7244/CPA
CURRENT APPLICATION NUMBER: US/C8/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/C22,689
PRIOR PILING DATE: 1996-07-26
NUMBER OF SEG 12 NOS: 38
SOFTWARE: FastSEQ for Windown:
                                                                                                                             99.94;
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                           Query Match
Best Local Similarity 99.8
Matches 584; Conservative
                                                                     ; MOLECULE TYPE: protein US-08-433-037-4
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US-08-897-956A-2
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LENGTH: 609
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CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN
RELATED PROTEINS
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APPLICATION NUMBER: US/08/448,196A FILING DATE: 23-MAY-1995 CLASSIFICATION: 530
                                                   Score 3095; DB 4;
Pred. No. 1.1e-285;
1; Mismatches 0;
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CITY: HUNTSVILLE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: CARTER, DAN
TITLE OF INVENTION:
TITLE OF INVENTION: BI
TITLE OF INVENTION: REL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NASA
STREET
                                                   Query Match
Best Local Similarity 99.8
Matches 583; Conservative
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COUNTRY: USA
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US-08-448-196A-3
US-08-897-956A-3
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                                                                                                                                                    99.9%; Score 3099; DB 5; Length 609; 99.8%; Pred. No. 2.4e-286; ive 1; Mismatches 3; Indels
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APPLICANT: Mary Ellen Digan.
APPLICANT: Mary Ellen Digan.
APPLICANT: Philip Lake
APPLICANT: Printin Lake
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38 NIGOWS Version 4.0
SEQ ID NO
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Patent No. 6423512
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                                                                                                                                                       Query Match
Best Local Similarity 99.8
Matches 584; Conservative
                                unknown
                                                   TOPOLOGY: unknown
MCLECULE TYPE: protein
TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
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TYPE: PRT
GRGANISM: HOMO
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                                                                                                                                                                                                                                                                                                                                                                                                    KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSGRFPKAEFAEVSKLVTDLTK 240
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Fater No. 5948609
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C
APPLICANT: HO, JOSEPH X
APPLICANT: RUKER, FLORIAN
ITTLE OF INVENTION: OXYGEN-TRANSPORTING ALBUMIN-BASED BLOOD REPLACEMENT ITTLE OF INVENTION: COMPOSITION AND BLOOD VOLUME EXPANDER
                                                                                                                                                                                                                                                             1 DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                          NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
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                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3093; DB 1;
Pred. No. 8.3e-286;
         NAME: BROAD JR., ROBERT L.
REGISTRATION NYBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-28432-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0021
TELEPHONE: 205-544-028
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                              99.7%;
ATTORNEY/AGENT INFORMATION
                                                                                                      : 585 amino acids
amino acid
                                                                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                             Query Match
Best Local Similarity 99.7
Matches 583; Conservative
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                       US-08-448-196A-3
                                                                                                       LENGTH:
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CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN
RELATED PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAHKSEVAHRFKOLGEENPKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                                                                                                                                                                                               61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
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                                                                                                                                                                                                 Length 585;
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                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                         Score 3093; DB 2;
Pred. No. 8.3e-286;
1; Mismatches 1;
CURRENT APPLICATION NUMBER: US/08/984.176
CURRENT FILING DATE: 1997-12-03
NUMBER CF SEQ ID NOS: 1
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: MARSHALL SPACE FLIGHT CENTER CITY: HUNTSVILLE STATE: ALABAMA ZIATE: ALABAMA ZIP: 358:2
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US-08-448-196A-5
Sequence 5, Application US/08448196A
Fatent No. 5780594
GENERAL INFORMATION:
APPLICANT: CARTER, DANIEL C.
TITLE OF INVENTION: BIOLOGICALLY ACTILE OF INVENTION: RELATED PROTEIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             99.7%;
                                                                                                                                                                                         Query Match
Best Local Similarity 99.7
Matches 583; Conservative
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61 NODKSLHTJEGDKLCTVATLRETYGBMADCCAKQEPBRNECFLOHKDDNPNLPRJYRPEY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 VHKECCHGDLLECADDRADLAKYICEHQDSISGKLKACCDKPLLQKSHCIAEVKEDDLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     79.2%; Score 2458.5; DB 1; Length 583; 75.8%; Pred. No. 2.1e-225; 1.ve 70; Mismatches 70; Indels 1;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOUTER: IBM PC compatible
OPERATING SYSTEX: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,196A
FILING DATE: 23-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BROAD JR., SOBERT L.,
REGISTRATION NUMBER: 18,757
REFERENCE/DOCKET NUMBER: XX/MFS-284,22-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 205-544-0228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.8
Matches 442; Conservative
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Inear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Searsh completed: October 27, 2003, 15:22:31

Job time : 31 secs

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NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: MBRI-02584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 585 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
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1, Appli
2, Appli
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Sequence 445, App
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Sequence 26, App.
                                                                                                                (without alignments)
1360.618 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 5, Apsequence 18, 7
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Sequence
Sequence
Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOXB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOXB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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3103
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                                                                                              October 27, 2003, 15:21:13; Search time 72 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-932-613-445
US-09-833-041-18
US-10-153-604A-5
US-10-119-263-2
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US-10-414-469-1
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US-10-413-831-2
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Maximum Match 100%
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SOURCES SOURCES: 2

CORESPONDENCE ADDRESS: 2

CORESPONDENCE ADDRESS: ADDRESSE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

CITY: San Francisco

STATE: California

COMPUTER: Rebable FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: RBM PC compatible

OPERATING SYSTEM: PC LODS/MS-DCS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURREY APPLICATION NUMBER: US/09/929,552

FILING DATE: 14 Ang-2001

PRIOR APPLICATION: CURROWN.

PRIOR APPLICATION ATPA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 04 ANG - 2001

FILLING DATE: 14 ANG - 2001

FILLING DATA:

PRIOR APPLICATION NUMBER: 04 ANG - 2001

FILLING DATA:

PRIOR APPLICATION NUMBER: 04 ANG - 2001

FILLING DATA:

PRIOR APPLICATION: VUMPER: 04 ANG - 2001

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PRIOR APPLICATION: VUMPER: 04 ANG - 2001

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US-10-237-667-2
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FILING DATE: 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sonnenschein, Carlos
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100.08;
Query Match
Best Local Similarity 100.
Matches 585; Conservative
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Sequence 445 Application US/09326:3
Fublication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belizer, W. Daniel
APPLICANT: Potter, W. Daniel
APPLICANT: Rosen, Craig A. Tony J.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREUN
FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 445
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                                                                                  Query Match 100.0%; Score 3103; DB 10; Best Local Similarity 100.0%; Pred. No. 2.4e-269; Matches 585; Conservative C; Mismatches 0;
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO:
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US-09-932-613-445
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Publication No. US200301C4578A1
GENERAL INFORMATION:
APPLICANT: BAllance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLPSJAADFVESKOVCKNYAEAKOVFJGMFLYEYARRHPDYSVVLLLRJAKTYETTLEKC
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CORRESPONDENCE ADDRESS:
ADDRESSES: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER,
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Score 3103; DB 11;
Pred. No. 2.4e-269;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,873
FILING DATE: 25-JUN-1998
APPLICATION NUMBER: PCT/GB96/03164
                                             0; Mismatches
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COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,010
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COUNTRY: USA
ZIP: 2005-33:S
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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61 NCDKSLHTLFSDKLCTVATJRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
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                                                                                                                                                                                                                                                                                  DB 11;
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Sequence 18, Application US/09833041
GENERAL INFORMATION:
APPLICANT: Hosen, Craig A.
APPLICANT: Rosen, Craig A.
ITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF545
CURRENT FILLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
             INFORMATION FOR SECTION TO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: SES amino acids
TYPE: amino acids
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
WOLECTLE TYPE: protein:
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 26
FILING DATE: 19-DEC-1996
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Publication No. US20030:43191A1
GENERAL INFORMATION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PFS.56
CURRENT APPLICATION NUMBER: US/10/153,604A
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SCHWARE: Patentin version 3.1
SEQ ID NO 5
LEBGTH: 585
                                                                                                                                                                                 Query Match
100.0%; Score 3103; D3 11;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Xatches 585; Conservative 0; Mismatches 0;
PRICE APPLICATION NUMBER: 60/199,384
PRICE FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 79
SCFUARE: Patentin Ver. 2.1
SEQ ID NO :8
LENGTH: 585
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ORGANISM: Homo Sapiens
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CRGANISM: Homo Sapiens
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                      Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative C; Mismatches 0;
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Sequence 18, Application US/0983317
Publication No. US20030171267A1
APPLICANT: Rosen, Craig A.
APPLICANT: Sadeghi, Homa
APPLICANT: Turner, Christopher P.
APPLICANT: Prior, Christopher P.
TILE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF543
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/259,358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-15
SOFTWARE OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
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ORGANISM: Homo Sapiens
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US-1C-17-26-31
Sequence 1, Application US/10319263
Publication No. US20030180820A1
SEXREAL INFORMATION:
PAPLICANT: Bar-Or M.D., David
APPLICANT: Lau Ph.D., Edward
APPLICANT: Lau Ph.D., Edward
APPLICANT: Winkler M.D., James V.
TTLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
TILLE OF INVENTION: Kits
TILLE OF INVENTION: Kits
FILE REPERENTE: ISCOO7
CURRENT FILING DATE: 2002-12-13
FRIOR APPLICATION NUMBER: 60/105,738
FRIOR APPLICATION NUMBER: 60/102,738
FRIOR APPLICATION NUMBER: 60/102,738
FRIOR APPLICATION NUMBER: 09/165,926
FRIOR APPLICATION NUMBER: 09/165,926
FRIOR APPLICATION NUMBER: 09/165,581
FRIOR APPLICATION NUMBER: 09/165,581
FRIOR APPLICATION NUMBER: 09/165,581
FRIOR PILING DATE: 1998-10-02
FRIOR FILING DATE: 1998-10-02
FRIOR PILING DATE: 1998-10-02
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Query Match 100.0%; Score 3103; DB 12; Length Best Local Similarity 100.0%; Pred. No. 2.4e-269; Matches 585; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
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Publication No. US20030190651A1
General Propertion No. US20030190651A1
General Propertion:
APPLICANT: Bar-Or No., David
APPLICANT: Bar-Or No., David
APPLICANT: Winkler M.D., Edward
APPLICANT: Winkler M.D., James V.
TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
TITLE OF INVENTION: Kits
FILE REFERENCE: ISCOO7
CURRENT FILING DATE: US/10/414,469
CURRENT FILING DATE: 1999-10-01
PRIOR PLICATION NUMBER: 60/115,392
PRIOR APPLICATION NUMBER: 60/115,392
PRIOR PLING DATE: 1999-01-11
PRIOR PLING DATE: 1999-01-11
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Pred. No. 2.4e-269;
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Best Local Similarity 100.0%; Pred. No. 2.4
Matches 585; Conservative 0; Mismatches
                    FEATURE:

NAME/KEY: MOD RES

LOCATION: (1) ... (585)

O'THER INFORMATION: ACETYLATION
US-10-319-263-2
     ORGANISM: Homo sapiens
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US-10-414-469-1
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| Sequence 2, Application US/10319263
| Sequence 2, Application US/10319263
| Publication No. US20030186820A1
| GENERAL INFORMATION:
| APPLICANT: Lau Ph.D., Edward
| APPLICANT: Lau Ph.D., Edward
| APPLICANT: Lau Ph.D., James V.
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION: Wist for the Rapid Evaluation of Ischemic States and
| TITLE OF INVENTION NUMBER: 60/105,392
| PRIOR FILING DATE: 1999-10-02
| PRIOR FILING DATE: 1999-10-02
| PRIOR FILING DATE: 1999-10-02
| WIMBER OF SEQ ID NOS: 2
| SOFTWARE: PATENTIN OF: 2.0
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                                      DB 12; Length 585;
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                                                                        Indels
                                                       2.4e-269;
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                                   100.0%; Score 3103;
100.0%; Pred. No. 2.
                                                                      Conservative
                                 Query Match
Best Local Similarity
Matches 585; Conserv
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LENGTH: 585
TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches C:
PRICE FILING DATE: 1999-10-01
PRICE APPLICATION NUMBER: 60/115,392
PRICE PILING DATE: 1999-01-11
PRICE PILING DATE: 1999-01-02
PRICE PRICE DATE: 1998-10-02
PRICE PRICE DATE: 1998-10-02
PRICE FILING DATE: 1998-10-02
PRICE FILING DATE: 1998-10-02
PRICE APPLICATION NUMBER: 09/165,926
PRICE APPLICATION NUMBER: 09/165,926
PRICE APPLICATION NUMBER: 09/165,581
PRICE FILING DATE: 1998-10-02
NUMBER OF SEC ID NOS: 2
SOFTWARE: PALCELLIN VEY: 2.0
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GENERAL INFORMATION: APPLICANT: Dyax Corp. APPLICANT: Beltzer, James P.
                                                                                                                                                                                                                                                         NAME/KEY: MOD_RES
LOCATION: (1)_.(585)
CTHER INFORMATION: ACETYLATION
US-10-414-469-2
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-09-932-322-445
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Publication No. US20030190691A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bar-Or M.D., David
APPLICANT: Lau Ph.D., Edward
APPLICANT: Hinkler M.D., James V.
TITLE OF INVENTION: Tests for the Rapid Evaluation of Ischemic States and
TITLE OF INVENTION: Kits
FILE REFERENCE: ISCG07
CURRENT FAPLICATION NUMBER: US/10/414,469

CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/US99/22905
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100.0%; Pred. No. 2.4e-269;
ative 0; Mismatches 0;
 PRIOR APPLICATION NUMBER: 09/165,326
PRIOR PILING DATE: 1980-10-02
PRIOR PELING DATE: 1990-10-02
PRIOR FILING DATE: 1990-10-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SEQ IP NO 1
TYPE: PRT
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Best Local Similarity 100.8
Matches 585, Conservative
                                                                                                                                                CRGANISM: Homo sapiens US-10-414-469-1
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Publication No. US20030194813A1
GENERAL INPORMATION:
APPLICANT: Bar-Or M.D., David
APPLICANT: Lau Ph.D., Edward
APPLICANT: Winkler M.D., James V.
TITLE OF INVENTION: Fests for the Rapid Evaluation of Ischemic States in TITLE OF INVENTION: Kits
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llarity 100.0%; Pred. No. 2.4e-269;
Conservative 0; Mismatches 0;
   PRIOR APPLICATION NUMBER: US/09/806,247
PRIOR PILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/115,392
PRIOR FILING DATE: 1999-01-1
PRICR FILING DATE: 1998-10-02
PRICR FILING DATE: 1998-10-02
PRICR FILING DATE: 1998-10-02
PRIOR PILING DATE: 1998-10-02
PRIOR PRICR TON NUMBER: 09/165,581
PRIOR PRICR OATE: 1998-10-02
PRIOR FILING DATE: 1998-10-02
PRIOR FILING DATE: 1998-10-02
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PRIOR FILING DATE: 1998-10-02
SCFTWARE: PATENTIN VEY: 2.0
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Best Local Similarity
Matches 585; Conserv
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US-10-413-831-2
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APPLICANT: Fleming, Tony J.
APPLICANT: Ladmer, Robert Charles
APPLICANT: Ladmer, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B L.
FILE REPRENCE: Dyx-018.1 PCT; DYX-018.1 US
CURRENT PAPLICATION UNMERR: US/09/932,322
CURRENT FILING DATE: 2001-08.17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: Patentin version 3.1
SEQ ID NO 445
LENGTH: 585
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Publication No. US2003019481341

GENERAL INFCRMATION:
APPLICANT: Bar-Or M.D., David
APPLICANT: Lau Ph.D., Edward
APPLICANT: Lau Ph.D., Edward
APPLICANT: Winkler M.D., James V.
TITLE OF INVENTION: Tests for the Rapid Eval
TITLE OF INVENTION: Kits
FILE REPERENCE: ISCOON
CURRENT FILING DATE: 2003-04-15
                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 585, Conservative
                                                                                                                                                                                                    TYPE: PRT
ORGANISM: HomoSapiens
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US-09-932-322-445
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Publication No. US20030104578A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION:
AND SERUM ALBUMIN
NUMBER OF SEQUENCES 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
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                    APPLICANT: Bell et al.
TITLE OF INVENTION:
APPLICANT: Bell et al.
TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
FILE REFERENCE: PF556
CURRENT APPLICATION NUMBER: US/10/153,364
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/293,212
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                             .
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100.0%; Score 3103; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.4e-269;
Matches 585; Conservative 0; Mismatches 0;
          US20020142814A1
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US-10-153-064-5
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US-09-984-010-7
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVMCTAPHDNEETFLKKYLYSIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 3103; DB 12; Length 585; 100.0%; Pred. No. 2.4e-269; tive 0; Mismatches 0; Indels 0;
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FILE REFERENCE: ISC007
CURRENT APPLICATION NUMBER: US/:0/413,831
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: US/09/806,247
PRIOR APPLICATION NUMBER: US/09/806,247
PRIOR FILING DATE: 1990-01-11
PRIOR PILING DATE: 1990-01-11
PRIOR PILING DATE: 1990-01-11
PRIOR FILING DATE: 1990-01-02
PRIOR FILING DATE: 1998-10-02
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MOD_RES

; LOCATION: (1)...(585)
; OTHER INFORMATION: ACETYLATION
US-10-4.3-831-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.
Matches 585; Conservative
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                 COUNTRY: USA
ZIP: 20005-3115
ZIP: 20005-3115
COMPUTER READABLE FORM:
MEDIJUT TYPE: Floppy disk
COMPUTER: 18P PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patemtin Release #1.0, Version #1.30 (BPD)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,013
FILING DATE: 21-MAy-2002
PRIOR APPLICATION NUMBER: US/09/994,013
FILING DATE: 25-UN-1998
APPLICATION NUMBER: US/09/091,873
FILING DATE: 19-DEC-1996
INFORMATION FOR SEC ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TVPE: amino acid
TVPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 3103; DB 11; Length 604;
Best Local Similarity 100.0%; Pred. No. 2.5e-269;
Matches 585; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
STREET: 1300 I Street, NW
               CITY: Washington
STATE: DC
COUNTRY: USA
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Search completed: October 27, 2003, 15:31:04 Joh time : 74 secs

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GenCore version 5.1.6
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Run

1308.341 Million cell updates/sec

....TCFAEEGKKLVAASCAALGL 585 US-09-833-117-18 3103 1 DAHKSEVAHRFKDLGEENFK. Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

96168682 residues

283308 seqs,

Searched:

DB seg length: 0 DB seg length: 200000000 Manimum Minimum Match 0% Maximum Match 100% Listing first 45 su Post-processing:

Summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

	Description		pre	bumin pre	bumin pre	bumin pre	prmin	bumin pre	albumin pre	albumin	albumin - Mongolia	alb	albumin pr	lpha-fetoprot	lpha-fetoprot	9	4K albumin prec	albumin - dog (fra	8K serum albumi	lpha-feto	pha-	amin r	rum albu	precurs	٠,	serum albumin 2 pr	١.	rum albu	din	tamin D-bindin	ınd
	ID		ABHUS	A47391	S57632	ABHOS	ABBOS	ABSES	ABRTS	ABPGS	JC5838	AC5139	ABCHS	JC4258	FPHU	FPGO	ABX172	146986	ABX168	FPMS	FPRT	A54906	859517	A53195	ABONS:	ABONS2	A37253	\$27941	VYHUD	VYRTD	A35327
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A71928	G64585	T30282	AG2558	JC2221	JC2300	T17272	S51364	T06733	352217	D35815	PC4035	JC4091	A64465	152330	A59236
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184	184	141.5	137.5	134.5	134	134	133.5	132.5	131	130	129	128.5	128	128	126.5

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N.Alcendate names: preproalbumin
N.Alcendate and are serviced by the service of t

A;Molecule type: mRNA
A;Residues: 1-419, "K.,421-609 <LAW>
A;Residues: 1-419, "K.,421-609 <LAW>
A;Cross-references: BEL:VO0495; GB:C00078; GB:C00132; GB:L00133; NID:g28591; PIDN:CF
A;Cross-references: BEL:VO0495; GB:C0078; GB:C00132; GB:L00133; NID:g28591; PIDN:CF
R;Dugaiczyk, A.; Law, S.W.; Dennison, O.E.
Froc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982
A;Title: Nucleoride sequence and the encoded amino acids of human serum albumin mRNA.
A;Reference number: A93936; MUID:82105994; PMID:6275391

A,Molecule type: mRNA
A,Residues: 1-120,/G',122-609 <DUG>
A)Residues: 1-120,/G',122-609 <DUG>
A)Cross-references: BMEL:VOCH94; NID:928589; PIDN:CAA23753.1; PID:928590
B;Urano, Y.; Watenabe, K.; Sakai, M.; Tamaoki, T.
J. Biol. Chem. 261, 3244-325; 1986
A;Ille: The human albumin gene. Characterization of the S' and 3' flanking regions & A;Reference number: I39427; MJD:86140099; PMID:2419329
A;Accession: I39427

A.Status: translation not shown A.Molecule type: DNA

A, Residues: 1-26 < URA>
A, Cross-references: GB-M13075; NID:g178330; PIDN:AAAS:688.1; PID:g553173
A, Cross-references: GB-M13075; NID:g178330; PIDN:AAAS:688.1; PID:g553173
B, Watkins, S.: Madison, J.; Galliano, M.; Minchlotti, L.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994
A, Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami A, Reference number: 159286; MUID:94181575; PMID:8134387
A, Accession: 159286

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA

A,Residues: 282-29C,'KSRFDLC' < WATS
A,Cross-references: GB:S69192, NID:946032, PIDN:AAB30282.1, PID:9546033
A,Cross-references: GB:S69192, NID:946032, PIDN:AAB30282.1, PID:9546033
A,Note: this frame-shift variant, designated albumin Roma, leads to analbuminemsa R,Madison, C.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putna Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994
A;Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox A;Reference number: I59313, MUD:94294404; PMID:8022807

A;Status: translated from GB/EMBL/DDBJ

A;Residues: 589-590,'AlpRRVKMLLLQVKLP' <MAD> A;Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232 A;Molecule type: DNA A;Residues: 589-590,'ALPRRVKWLLLQVKLP'

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A; Molecule type: protein
A; Residues: 255-263, "E', 265-281 <MINI>
A; Residues: 255-263, "E', 265-281 designated albumin Herborn
R; Mince: this variant is designated albumin Herborn
B; Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Pol
B; Ochim. Biophys. Acta 1119, 232-238, 1992
A; Title: Two alloalbumins with identical electrophoretic mobility are produced by dif
A; Reference number: S21078; MUID:92190239; PMID:1347703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 354-356, K,,358-378 <MIN2>
A;Note: Navariant is designated albumin Sondrio; another variant Paris-2 is repor:
A;He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
                                                                                                                                                                                  A.Title: The structural characterization and bilirubin-binding properties of albumin A.Reference number: S33298; MUID:93292504; PMID:8513793
A.Accession: S33298
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Am. J. Hum. Genet. 35, 565-572, 1983
A.Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein g
A.Reference number: A90028; MUID:83279982; PMID:6192711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicyclic R:Bohney, J.P.; Fonda, M.L.; Feldhoff, R.C. FEBS Lett. 298, 266-268, 1992
A;Title: identification of Lys(190) as the primary binding site for pyridoxal 5'-pho A;Reference number: A56294; MUID:9218381; PMID:1544460
A;Contents: annotation
A;Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesi
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (w
C:Comment: A large number of variants of human serum albumin have been described.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4q11-4q13
C;Superfamily: serum albumin; serum albumin repeat homology
C;Kywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyr
E;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involved in high-affinity bind
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A;Title: Lysine residue 199 of human serum albumin is modified by acetylsalicyclic
A;Reference number: A46755; MUID:76257808; PMID:955675
A;Contents: annocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Affile: Atomic structure and chemistry of human serum albumin. A.Reference number: A46756; MulD:9233447; PMID:1630489
A.Reference number: A46756; MulD:9233447; PMID:1630489
A.Contentes annotation, X-ray crystallography, 2.8 angstroms
R.Brown, J.R.; Shockley, P.; Behrans, P.Q.
in The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 171, 453-459, 1978
A/TILLE: Lysine residue 240 of human serum albumin is involved in high-a-A/Reference number: A90299; MUID:78186630; PMID:656055
A/Contents: annotation; bilitubin-binding site
R/Perers, T.; Reed, R.G.
In Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjoholm, A/Reference number: A94408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Contents: annotation; three-dimensional structure and disulfide bonds R:Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B. Collect Czech. Chem. Commun. 42, 564-579, 1977
A:Title: Disulfide bonds in human serum albumin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .25-609/Product: serum albumin #status experimental <MPT>.29-202/Domain: serum albumin repeat homology <SA:>
    A;Residues: 76-83, K', 85-106 <GAL3.
A;Note: this variant is designated albumin Torino.
A;Note: this variant is designated albumin Torino.
Bur. J. Biochem. 214, 437-444, 1993
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R,Walker, J.E.
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                                                                                                                                                                                                                                                                                                                     A;Residues: 1-120,/G',122-455 <MEN>
A;Cross-references: EMBL:U22961; NID:g763428; FIDN:AAA64922.1; PID:g763431
A;Cross-references: EMBL:U22961; NID:g763428; FIDN:AAA64922.1; PID:g763431
B;Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J 308, 321-325, 1995
A;Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast Kexz A;Reference number: S55314; MUID:95275251; PMID:7755581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.F. Frich, J.W.; Crouch, R.K.; Knapp, D.R.; Schey, K.L.
Arch. Biochem. Biophys. 305, 559-599, 1993
Arch. Biochem. Biophys. 305, 559-599, 1993
A.;Tulle. Mass spectrometric identification of modifications to human serum albumin treat
A.;Reference number: $36892; MJID:93384321; PMID:8373158
A.;Accession: $36882
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A;Residues: 45-67;141-16C;311-337;469-490;570-581 <FIN>
K;Rassler, E.; Spiteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A;Title: Bruchstuecke aus Albumin und beta(2)-Wikroglobulin - Bestandteile der Wittelmol A;Reference number: S17599; MUID:92126241; PMID:1772598
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A;Residues: 166-173 <CAR>
R;Residues: 166-173 <CAR>
R;Rogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
Biochem. Biochem. Biochem. Securence of Kinetensin, a novel peptide isolated from pepsin-tre
A;Reference number: A03239; MUID:86242180; PMID:3087352
A;Accession: A03239
A;Note: this frame-shift variant is designated albumin Bazzano; four additional variants
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A;Residues: 25-54;354-31-447 <KAJ>
A;Residues: 25-54;354-3504-36
A;Note: 49-Leu was also found
B;Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J mamunoi. 143, 1680-1684, 198
A;Title: Structures of histanine-releasing pept.des formed by the action of acid process
A;Reference number: A45600; MUID:89341406; PMID:2474609
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A;Reference number: S06422
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A.Residus: 25-117, FEC, 126-154, Q',i56-193,'E',195-387,'H',389-390,'Y',392-393,'A',395-
R.Rochr, Us.; Spiteller, D.
Justus Liebigs Ann. Chem. 9, 881-884, 1988
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A; Molecule type: protein
A; Residues: 166-113, L. C. (MOG)
A; Residues: 166-113, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, Broc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A; Title: Mitations in genetic variants of human serum albumin found in Italy.
A; Reference number: A38255; MUID:91062352; PMID:2247443
A; Accession: C38255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 19-27 < LED>
KR,Meloun, B.; Mosavek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A,Title: Complete amino acid sequence of human serum albumin.
A,Reference number: A91420; MUID:76187907; PMID:1225573
A,Recession: A91420
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A;Accession: S06422
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A;Note: this variant is designated albumin Vibo Valentia
                                                   R;Menaya, J.; Parrilla, R.; Ayuso, M.S.
submitted to the EMBL Data Library, March 1995
A;Reference number: G08292
                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Residues: 82-105,'K',1
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CyAccession: Uq4660; S57632

R;Hilger, C.; Grigioni, F.; Hentges, F.
Secession: Uq4660; S57632

R;Hilger, C.; Grigioni, F.; Hentges, F.
Secession: Uq4660; MUID:96194824; PMID:8647469

A;Atle: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
A;Accession: Uq4660

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                                                94.8%; Score 2942; DB 2; Length 600.
93.5%; Pred. No. 4e-187;
live 23; Mismatches 15; Indels
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Species: Felis silvestris carus (domestic cat)
Pate: 19-oct-1995 #sequence_revision 03-Nov-1995 #text_change
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F;405-584/Domain: serum albumin repeat homology <SA3>
                                                Query Match
Best Local Similarity 93.5%
Matches 545; Conservative
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Kyarkhirs, S.; Sakameto, Y.; Madison, J.; Davis, B.; Smith, D.G.; Dwulet, J.; Putnam, F. Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993

A/Title: cDNA and protein sequence of polymorphic macaque albumins that differ in biling A/Reference number: A47391; MUD:93211971; PMID:8460152

A/Contents: B/B homozygote
A/Accession: A47391
                  F)221-394/Domain: serum albumin repeat homology <SA2>
F)413-592/Domain: serum albumin repeat homology <SA3>
F)27/Binding site: copper (Fis) #status predicted
F)27/Binding site: copper (Fis) #status predicted
F)77-86,99-115,114-125,148-191,192-201,224-270,269-277,289-303,302-313,340-385,384-393,F)214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLPSLAADFVESKDVCKNYABAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYSTTLEKC
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A/Molecule type: mRNA, protein
A/Residues: 1-600 <MAT>
A/Cross-references: GB:M90463; NID:g342294; PIDN:AAA36306.1; PID:g342295
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                                                                                                                                                                                                 Length 609;
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kinetensin #status experimental <KIP>
                                                                                                                                                                                           Query Match 100.0%; Score 3103; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.2e-198;
Matches 595; Conservative 0; Mismatches 0;
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Accession: Ababa; Notice to the preproal bumin

Nile trade names: 67K protein; preproal bumin

Cipecies: 80s primigenius taurus (cattle)

Cipecies: 80s primigenius taurus

Cipecies: 80s primigenius taurus

Cipecies: 80s primigenius taurus

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  Length
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Score 2475.5; EB Pred. No. 3e-156;
                                                   Mismatches
                                                   69
79.8%;
76.3%;
Query Match
Best Local Similarity 76.33
Matches 445; Conservative
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: 1-607 < EDA
A; Cross-references: 0B:X74645; MID:9399671; FIDN::CAA52194.1; PID:9399672
C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds capper, crevide hormones (weak bonds with these hormones promote their transfer across the membra C; Superfamily: serum albumin. serum albumin repeat homology
C; Keywords: carrier protein; duplication, metal binding; plasma
F; 1-18/Domain: signal sequence #status predicted <S:G>
F; 1-18/Domain: serum albumin #status predicted <AT>
F; 25-607/Product: serum albumin repeat homology <SAI>
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F;220-393/Domain: serum albumin repeat homology <SA3>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;27-86;99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,
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                                                                                                                                                                                                                                                                NCEKSLHELLGDKLCTVASLRDKYGEMADCCEKKEPERNECFLOHKDONFGFGOLVTPEA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serum albumin precursor - horse
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Date: 31-30e-1993 #sequence_revision 31-30e-1993 #text_change 22-Jun-1999
C;Accession: 534053
R;Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, F.D.; Carter, D.C.
Blur, J.S. Blochem, 218, 205-212, 1993
A;Title: X-ray and primary structure of horse serum albumin (Equus caballus)
A;Reference number: 534053; MUD:93345495; PMID:8344282
                                                                                                           DAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE 60
                                                                                                                                            LVNRRPCFSALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELKHKPKAT
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  84.4%; Score 2625; DB 2; 82.0%; Pred. No. 8.2e-166; ive 52; Mismatches 53;
  Query Match
Best Local Similarity 82.0%
Matches 478; Conservative
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240

84

Gaps

420

443

480

540

Length 607;

DB 1;

Score 2432.5;

78.48;

Query Match

DB 1.

Score 2446.5;

78.8%;

Query Match

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Cystoperfamily: serum albumin; serum albumin repeat homology
Cystoperfamily: serum albumin; serum albumin repeat homology
Cystoperia: signal sequence #status predicted <515>
Fil-19-24/Jocaain: signal sequence #status predicted <516>
Fig-2-607/Product: serum albumin #status predicted <MAT>
Fig-20-201/Domain: serum albumin repeat homology <5A1>
Fig-20-393/Domain: serum albumin repeat homology <5A2>
Fig-20-393/Domain: serum albumin repeat homology <5A3>
Fig-591/Domain: serum albumin repeat homology <5A3>
Fig-591/Domain: serum albumin repeat homology <5A3>
Fig-591/Domain: serum albumin repeat homology <5A3>
Fig-591/Jonain: serum albumin repeat homology <5A3>
Fig-591/Jonain: serum albumin repeat homology <5A3>
Fig-591/Jonain: serum albumin repeat homology <5A3>
Fig-591/Binding site: copper (His) #status predicted
Fig-7-66,99-115,114-125,147-192.191-200,223-269,268-276,288-302,301-312,339-384,383-35;
Fig-60-115,114-125,114-125,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135,114-135
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A.Mclecule type: mRNA
A.Residues: 1-607 - SERD-
A.Residues: 1-607 - SERD-
C.Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppeteroid hormones (weak bonds with these hormones promote their transfer across the men
                                                                                                                                                                                                                                                                                    6. NCDKSLHTLFGDKLCTVATLRBTYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
                                                                                                                                                                                                                                                                                                                                85 GCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKL-KPDP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DUMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCOAADKAACLLP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VATECCHGDILECADDRADLAKYICENQDSISSKLKECCEKPILEKSHCIAEVENDEMPA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPSIAADFVESKOVCKNYAEAKOVFLGMFLYEYARRHPDYSVVLLIRLAKTYETTLEKC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 LVNRRPCFSALTPDETYVPKAFDEKLFTFHADICTLPDTEKQIKKOTALVELLKHKPKAT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 NTLCDEFKADEKKFWGKYLYBIARRHPYFYAPELLYYANKYNGVFQDCCGAEDKGACLLP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 VHKECCHGDLLECADDRADLAKYICDNODTISSKLKECCOKPULEKSHCIAEVEKDAIPE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 PILVEVSRSLGKVGTRCCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTES 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RiBrown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A;Reference number: S06936; MUID:90098888; PMID:2602160
                                                                                                                         DAHKSEVAHRPKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                                                                              KLDELRDEGKASSAKORLKCASLOKFGERAFKAWAVARLSORFPKAEFARVSKLVTDLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic she
C;Date: 31-Dec-1993 #sequence_revision 11-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQLKTVMENFVAFVDKCCAADDKEACFAVEGPKLVVSTQTAL 606
                                                        Irdels
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            2.5e-154;
                                                        Mismatches
            Pred.
                                                71;
            75.68;
                                                        Conservative
        Best Local Similarity
Matches 441; Conserv
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A,Residues: 25-41,'H',43-117,'EQ',123-179,181-189,'E',191-194,'A',196-213,'T',215-288,'E
R,Brown, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Reference number: A91457
A; Contents: annotation; disulfide bonds
A; Contents: annotation; disulfide bonds
B; Werlen, R.C.; Officer, R.C.;
Biochem, J. 302, 907-911, 1994
A; Title: Preparation and characterization of novel substrates of insulin proteinase (EC A; Reference number: S55232; MUID:95031935; PMID:7945213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,
                                                                                 Anal. Biochem. 170, 1-9, 1988
A;Title: Electroblotting onto glass-fiber filter from an analytical isoelectrofocusing
A;Reference number: A60808; MuID:88267456; PMID:3389500
A;Accession: E60808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 163-172 <CAR>
R;Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from A;Reference number: A26693; MUID:87134805; PMID:2437111
                                                                                                                                                                                                                                                                            A;Residues: 25-41 <HSI>
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is A;Reference number: S10780; MUD:90336641; PMID:2379503
A;Reference number: S10780
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A;Residues: 165-172, 5, <CA2>
R;Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Bj.chem. J. 191, 867-868, 1980
A;Title: Sequence of residues 400-403 of bovine serum albumin.
A;Reference number: A90309; XJID:82023364; PMID:7283978
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A;Molecule type: protein
A;Residues: 529-536;569-572 < WPR>
C;Superfamily: serum albumin; serum albumin repeat homology
C;Superfamily: serum albumin; serum albumin; duplication; p.
C;Keywords: carrier protein; copper binding; duplication; p.
F;1-18/Domain: signal sequence #status experimental < S:G>
F;19-24/Domain: propeptide #status experimental < PRO>
F;25-607/Product: serum albumin #status experimental < MPT>
F;25-607/Product: serum albumin #status experimental < MPT>
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1220-393/Domain: serum albumin repeat homology <SA2>
1412-591/Domain: serum albumin repeat homology <SA3>
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A; Residues: 25-41, 'H' 43-57, 59-64 <STR>
B; Carraway, R.E.; Cochrane, D.E.; Boucher, J.
J. Immunol. 143, 1680-1684, 1989
A; Title: Structures of histamine-releasing A; Reference number: A45800; MUID:893414066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fed. Proc. 34, 591, 1975
A,Title: Structure of bovine serum albumin.
A,Reference number: A91458
A,Accession: A91458
A;Residues: 1-32 <WAG>
R;Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
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A,Reference number: A94551
A,Accession: A94551
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Fed. Proc. 33, 1389, 1974
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A;Residues: 190-195 <BR2>
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A,Residues: 402-433 <REE>
                                                                                                                                                                                                                                               A; Molecule type: protein
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A;Residues: 25-222 <1S1>
B;Isemura, S.; Ikenawa, T.
Bischem. 79, 1183-1196, 1976
A;Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amin A;Reference number: A91940; MUID:76260153; PMID:956149
A;Reference number: A91940
A;Rolecule type: protein
A;Residues: 223-2885;72-608 <1S2>
A;Rote: 262-Leu was also found
B;Residues: 223-288;72-608
A;Rote: 262-Leu was also found
A;Residues: 283-38486, T.; Indiaa, F.
B;Acyagi, Y.; Krenaka, T.; Indiaa, F.
A;Rote: 262-Leu was also found
A;Residues: 38, 3483-3486, 1978
A;Title: Copper(II)-binding ability of human alpha-fetoprotein.
A;Reference number: A90758; MUID:7901617; PMID:50265
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                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Structures of histamine-releasing peptides formed by the action of acid prot
A,Reference number: A45800; MUID:89341406; PMID:2474609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;27/Sinding site: copper (His) #Status experimental
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 JVMCTAPHDNEETFLKKYLYBIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Biol. 7, 2425-2434, 1987

A;Title: Determinants of rat albumin promoter tissue specificity analyzed ?
A;Reference number: I57621, MUID:87286876; PMID:3475566
A;Accession: I57621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-5 «RES»
A.Gross-references: 08:Mi6825; NID:g202828; PIDN:AAA46712.1; PID:g554412
C.Superfamily: serum albumin; serum albumin repeat homology
C.Superfamily: serum albumin; duplication; metal binding; plasma
F.1-14/Domain: signal sequence #status experimental «RC»
F.25-608/Product: serum albumin #status experimental «MAT»
F.25-608/Product: serum albumin repeat homology «SAI»
F.21-394/Domain: serum albumin repeat homology «SAI»
F.21-394/Domain: serum albumin repeat homology «SAI»
F.21-304/Domain: serum albumin repeat homology «SAI»
F.21-304/Domain: serum albumin repeat homology «SAI»
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R.Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.
J. Immunol. 143, 1680-1684, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2426; DB 1;
Pred. No. 5.6e-153;
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Best Local Similarity 73.4%;
Matches 428; Conservative 8:
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 166-173 <CAR>
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A,Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavag
A,Reference number: A91946; MUID:78109429; PMID:564345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of the pre-piece. Analys
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A. Molecule type: mRNA
A. Molecule type: maturation
A. Molecule type: maturation
A. Molecule type: maturation
A. Molecule type: maturation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKOTALVELVKHKPKAT 540
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NyAlternate names: preproalbumin
C;Species: Rattus novegicus (Norway rat)
C;Species: Rattus novegicus (Norway rat)
C;Species: 31-May-1979 #sequence revision 31-May-1979 #text_change 22-Jun-1999
C;Accession: A93872; A92211; A91946; A91940; C45800; I57621; A03233
R;Sargent, T.D.; Yang, M.; Bonner, Ö.
Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981
Proc. Natl. Acad. Sci. U.S.A. 78, C43-246, 1981
A;Ribe: Nucleolide sequence of cioned rat serum albumin messenger RNA.
A;Reference number: A93872; MUID:81223722; PMID:7017712
                                                                                                                                                                                                                            GCDKSCHTLFGDELCKVATLRETYGDMADCCEKQEPERNECFLNHKDDSPDLPKL-KPEP
                                                                                          DAHKSEVAHRFKOLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                                                                                                                       61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                                                                                                                                                                                                                               DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP
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                                       Gaps
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pred. No. 2.1e-153;
                                       73; Mismatches
                  75.0%;
                                       Conservative
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A;Residues: 1-38 <STR>
R;Isemura, S.; Ikenaka, T.
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Molecule type: protein
             Best Local Similarity
Matches 437; Conserv
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Db 262 VHKECCHGDLLECADDRADLAXYICENQDTISTKLKECCDKFLLEKSHCIAEAKRDELPA 321 Qy 301 DLPSLAADFVESKDVCKNYAEAKDVFLGMELYEYSVKULLRLAKTYETTLEKC 360 122 DLNPLEHDFVEDKEVCKNYKEAKDVFLGTFLYEVSRHPDYSVSLLRIAKTYETTLEKC 381 Cy 361 CAAADPRECYAKVPDEFKDVEDFKDVELKGTFEDGGSYFGNALLVRYTKV9QVST 422	29 491 LINARROCESALENDETPERADICTISEKEROTKKOTALVELYWERPAT 543 ED 532 LUNBERCFSALENDETFERADICTISEKEROTKKOTALVELYWERPAT 561 20 541 KEDLKAVKUDPAAFVEKCCKADKETCRAEGOKLY 576 542 KEDLKAVKUDPAAFVEKCCKADKETCRAEGOKLY 576 542 KEDLKAVKUDPAAFVEKCCKADKETCRAEGOKLY 576 543 KEDLKAVKUDPAAFVEKCCKADKETCRAEGOKLY 576 544 KEDLKAVKUDPAAFVEKCCKADKETCRAEGOKLY 576 552 EQUKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 552 EQUKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 554 EQUKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 555 EQUKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 556 EGOKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 556 EGOKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 557 EGOKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 558 EGOKTYLONFAAFVEKCCKADKETCRAEGOKLY 576 558 EGOKTYLONFAAFVEKCCKADKETCRAEGOKLY 577 559 EGOKTYLONFAAFVEKCCKADKETCRAEGOKLY 577 550 EGOKTYLONFAAFVEKCCKATARETYCERAEGOKLY 577 550 EGOKTYLONFAAFVEKCCKATARETYCERAEGOKLY 577 551 EGOKTYLONFAAFVEKCCKATARETYCERAEGOKLY 577 552 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKLY 578 554 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKLY 578 555 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKLY 578 556 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKLY 578 557 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKLY 578 558 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKRY KAAFTECCCAADKAACTLEK 191 557 AAKSENTAEGOKLY 588 558 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKRY KAAFTECCCAADKAACTLEK 191 557 AAKSENTAEGOKLY 588 558 EGOKTYLONFAAFVEKCKSKYKKETERAEGOKRY TOTOCKYTAETCRAEGOKRY TOTOCKYTAETCRAEGOKR	Oy 302 LPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLRLAKTYETTLEKCC 361
421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480 445 PTLVEAARNLGRVGTKCCTLPEAQRLPCVEDYLSAILNRLCVLHEKTPVSEKVTKCSSS 504 481 LVNRRPCFSALEVDETYVPKEFNAETFFHADICTLSEKERQIKKQTALVELVKHYRKAT 540 505 LVNRRPCFSALTVDETYVPKEFKAETFFHSDICTLPEKERQIKKQTALVELVKHYRKAT 564 607 S41 KEQLKAVKDDFAAFVEKCCKADDKETCFAEGKKLVAASGAAL 583 618 EDQLKTVMGDFAAFVEKCCKADDKETCFAEGKKLVAASGAAL 583 619 S65 EDQLKTVMGDFAAFVEKCKADDKETCFAEGRKLVAASGAAL 583 656 EDQLKTVMGDFAAFVEKCKADDKETCFAEGRKLVAASGAAL 583	cions of mi tions of mi tross the mi cross the mi s 1; s 1; s 1; s 1; s 1; s 1; s 1; t binds cop cross the mi de 60 t binds cop cross the mi	- n X-X 4-

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Oy 495 ETYVPKEFNAETFTFHADICTLSEKEROIKKOT 527 Db	albumin precur cles: Gallus ga e: 31-Dec-1993 ession: S15571; sady, A.I.; Sal tted to the EME	A;Reference number: S1551 A;Accession: S15571 A;Accession: S15571 A;Accession: S15571 A;Residues: 1-615 < CA35 A;Residues: 1-615 < CA35 A;Cross-references: EMBL:X60689; NID:g63747; PIDN:CAA43098.1; PID:g63748 B;Hache; R.J.G.; Wiskocill, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G. J. Bloù. Chem. 258, 4556-4564, 1983 A;Title: The 5' noncoding and flanking regions of the avian very low density apolige	AKETECE NUMBER: AUSU/8; MUID:8318103/; PMID:818//3/ A;ACCESSION: ACGOT8 A;Molecule type: DNA A;Restiucs: i.28 cHAC. A;Cross-references: GB:V00381; NID:g63038; PIDN:CAA23680.1; PID:g63039 B;Rosen, A.M.; Geller, D.M. Biochem: Biochys: Res. Commun. 78, 1060-1066, 1977 A;Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin. A;Reference number: Al3451; MUID:78019943; PMID:911327	A;Accession: Al1451 A;Motecule type: protein A;Resduce: 19-23,"M' 25-30 <ros> C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppendes (weak bonds with these hormones promote their transfer across the membranes), C;Superfamily: serum albumin, serum albumin repeat homology C;Keywords: carrier protein; duplication; metal binding; plasma F;10-18/Domain: signal sequence #status predicted <sig> F;27-613/Product: serum albumin #status predicted <anc></anc></sig></ros>	F:32-206/Domain: serum albumin repeat homology <sa1> F:225-398/Domain: serum albumin repeat homology <sa2> F:417-596/Domain: serum albumin repeat homology <sa3> F:3417-596/Domain: serum albumin repeat homology <sa3> F:32/Binding site: cooper (His) #status predicted F:32/Binding site: cooper (His) #status predicted F:80-89;102-118,117-128,152-197,196-205,228-274,273-281,293-367,306-317,344-389,388</sa3></sa3></sa2></sa1>	Length 615; Indels 1: Gaps	3 HKSEVAHRPKDLGEBNFKALVLIAFAQYLQCPFEDHVKLVNEVTEFAKTCVADESAENC [DE 90 SKFLPSIILDEICQVEKLRDSYGAMADCCSKADPERNECFLSFKVSQPDFVQPYQRPASD 149 QY 122 VMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPK 181	210 E1WAREKAKGVSVKOOYFGGILKQFGDRVPQARQLIYLSQKYPKAPFSEVSKFVHDSIGV 242 HTBCCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPAD 242 HTBCCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPAD 270 HKBCCEGGDMVECMDDMARMMSNLCSQQDVFSGKIKDCCEKPIVERSQCIMEAEFDEKPAD 302 LDSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCC
OY 422 TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNGLCVLHEKTPVSDRVTKCCTESL 481 447 TLVEARSLGRVGTHCCALPERKRLPCVEDYLSAILNRVCLLHEKTPVSEQVTKCCSGSL 506 QY 482 VNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELKRATK 541	Qy S42 EQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583	A05139 serum albumin - mouse (fragment) c:Species: Mus musculus (house mouse) c:Species: Mus musculus (house mouse) c:Date: 05-Jun-1987 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C;Accession: A05139, I48638 R:Minghetti, P.P.; Jaw, S.W.; Dugaiczyk, A. Mol. Biol. Evol. 2, 347-358, 1985 A;File: The rate of molecular evolution of alpha-fetoprotein approaches that of pseudog	A; Reference immune immune A; Parcession: A05139 A; Molecule type: mRNA A; Residues: 1-418 AMIN- A; Cross-references: GB M16111; NID:g191764; PIDN:AAA37190.1; PID:g191765 A; Cross-references: GB M16111; NID:g191764; PIDN:AAA37190.1; PID:g191765 B; Boccaccio, C.; Deschatrette, J.; Meunier-Rotival, M. Gene 88, 181-186, 1990 A; Tile: Bmpty and occupied insertion site of the truncated LINE-1 repeat located in the A; Reference number: I48638; MULD:9026606; PM101971802	A.Accession: 146638 A.Status: preliminary; translated from GB/EMBL/DDBC A.Status: preliminary; translated from GB/EMBL/DDBC A.Molecule type: DNA A.Residues: 379-453 <boc> A.Cross-references: EMBL:X13060; NID:952939; PIDN:CAA31458.1; PID:9899334 A.Cross-references: EMBL:X13060; NID:952939; PIDN:CAA31458.1; PID:9899334 C.Superfamily: serum albumin; serum albumin repeat homology (fragment) <sai> F;12104/Domain: serum albumin repeat homology (fragment) <sai> F;312-453/Domain: serum albumin repeat homology <az2></az2></sai></sai></boc>	Gaps	Qy 75 CTVATLRETYGEMADCCAKQEPERNECFLQHKDONPNLPRIVRPEVDVMCTAFHDNETF 134	### ##################################		241 VCRWYABARDVFLGTFLYBYSRRHPDYSVSLLLRLAKKYBATLEKCCAEANPPACYGTVL 30C QY 375 DEFKPLVBEPCNLIKQNCELFEQLGEYKFONALLVRYTKKVPQVSTPTLVBVSRNLGKVG 434

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A,Molecule type: protein
A,Residues: 19-45,60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
R,RGCCC, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
B.; McC., Med. Allied Sci. 34, 213-216, 1990
A,Title: Characterization of in vitro expressed human alpha-fetoprotein as highly re;
A,Reference number: A61480; MUID:91225826; PMID:1709209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X16110; NID:g773678; PIDN:AAB58754.1; PID:g178236
R;XCVey, J.H.; Michaelides, K.; Hansen, L.F.; Ferguson-Smith, M.; Tilghman, S.; Krum
Hum. Mol. Genet. 2, 379-384, 1993
A;Title: A c>A substitution in an HNF I binding site in the human alpha-fetoprotein
A;Reference number: S37655; MUD:93278385; PMID:7684942
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N.Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin
C.Species: Home saphens (man)
C.Species: Home saphens (man)
C.Date: 19-Feb-1984 #sequence revision 19-Feb-1984 #text_change 08-Dec-2000
C.Accession: A26624; S37655; A93961; A91497; A23699; A61480; A90624; A90757; A93042;
R.Gibbs, P.B.M.; Ziellinski, R.; Boyd, C.; Dugaiczyk, A.
Hiochemistry 26; 1332-1343; 1987
A;Title: Structure, polymorphism, and novel repeated DNA elements revealed by a comp
A;Reference number: A26624; MUID:87185438; PMID:243661
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A; Residues: 429-556 GB:20076
A; Cross-references: GB:20076
B; Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.
Biochemistry 30, 5061-5066, 1991
A; Title: Munan alpha-fetoprotein primary structure: a mass spectrometric study
A; Reference number: A23699; MUID:91242409; PMID:1709910
EKPECLSPNIANFLGDRDFNOFSSGEKNIFLASFVHEYSRRHPQLAVSVILRVAKGYQEL 380
                                                                                                   LEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEGLGEYKFQNALLVRYTKKVP 416
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                                                                                                                                                                                                                                                                                                                                                             CTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHK 536
                                                                                                                                                                                                                                                                                            OLISSELMAITRIMAATAATCCOLSEDKLLACGEGAADIIIGHLCIRHETTPVNPGVGQC
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A;Cross-references: GB:J00077; NID:g3:1348; PIDN:CAA24758.1; PID:g31351
A;Cross-references: GB:J00077; NID:g3:1348; PIDN:CAA24758.1; PID:g31351
B;Beattie, W.G.; Dugaiczyk, A.
Gene 20, 415-422, 1982
A;Title: Structure and evolution of human alpha-fetoprotein deduced from A;Reference number: A91497; MUID:83158778; PMID:6187626
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A, Residues: 1-28 <MCV-A
A, Residues: 1-28 <MCV-A
A, Cross-references: EXBL:Z19532; NID:g28527; PIDN:CAA79592.1; PID:g28528
A, Note: the authors translated the codon TAT for residue 26 as Thr
R, Morinaga, T.; Sakai, M.; Wegmann, T.G.; Tamaoki, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 4604,4608, 1963
A;Title: Primary structures of human alpha-fetoprote:n and its mRNA.
A, Reference number: A93961; MUID:83273664; PMID:6192439
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A, Molecule type: protein
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A; Residues: 1-609 <GIB>
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A)Introns: 291; 4612; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 436/2; 476/3;
C)Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: glycoprotein
F;I-19/Domain: signal sequence #status predicted <SIG>
F;20-609/Product: alpha-fetoprotein #status predicted <MAT>
F;20-202/Domain: serum albumin repeat homology <SAI>
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A;Cross-references: GB:U21916; MID:g841311; PIDN:AAA91641.1; PID:g841312
C;Comment: This protein is a plasma protein produced in the fetal and necratal liver
o similar properties and structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-fetoprotein precursor - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Accession: 37-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 20-Aug-1999
C;Accession: 37428
R:Nishio, H.; Gibbs, P.E.M.; Xinghetti, P.P.; Zielinski, R.; Dugaiczyk, A.
Gene 162, 213-220, 1995
A;Title: The chimpanzee alpha-fetoprotein-encoding gene shows structural similarity:
A;Reference number: JC4258; MJID:96032345; PMID:7557431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETT 356
                                                                                                                                                                                                                                  ANRRPCFTAMGVDTKYVPPPFNPDMFSFDEKLCSAPAEEREVGQMKLLINJIK3KPQMTE 569
                                                                                                                              KTDNPAECYANAGEGLNQHIKETQDVVKTNCDLLHDHGEADFLKSILTRYTKKYPQVPTD 449
                                                                                                                                                                                                   TLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESL 481
                                                                                                                                                                                                                                                                                                                                 VNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKGTALVBLVKHKPKATK 541
   LPSLVEKYIEDKEVCKSFEAGHDAFMAEFVYEYSRRHPEFSIQLIMRIAKGYESLLEKCC 389
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                                                                 AAADPHECYAKVFDEFKPLVEEPQNIIKQNCEIFEQLGEYKFQNALLVRYTKKVPQVSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQLIKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL
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A/Map position: 4q11-12
A/Introns: 29/1; 46/2; 90/3; 161/2: 206/3; 238/2; 281/3; 353/2; 397/3; 436/2; 476/3; 6/3 partens: 29/1; 46/2; 90/3; 161/2: 206/3; 238/2; 281/3; 353/2; 397/3; 436/2; 476/3; 6/5 partens: 29/1; 46/2; 90/3; 161/2: 206/2/2 partens abunin: serum albumin: glyoprotein; metal binding; plasma Fil-18/Domain: signal sequence #status predicted <516</td>

//record for signal sequence #status predicted <ART>
Fil-18/Domain: serum albumin repeat homology <531>
Fil-21: 394/Domain: serum albumin repeat homology <532>
Fil-3592/Domain: serum albumin repeat homology <532>
Fil-3592/Domain: serum albumin repeat homology <533>
Fil-3592/Domain: serum albumin repeat homology <533>
Fil-3592/Jomain: serum albumin repeat homology <533>
Fil-3692/Jomain: serum albumin rep
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                                                                                                                                 CLLPKLDEIRDEGKASSAKQRIKCASIQKFGERAFKAWAVARISGRFPKAEFAEVSKLVT
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A; Molecule type: protein
A; Mesidues: 'S'. 20-24, 'O'. 26-30, 'A', 32-35, 'E', 37-39 < RUC>
A; Residues: 'S'. 20-24, 'O'. 26-30, 'A', 32-35, 'E', 37-39 < RUC>
A; Residues: 'S'. 20-24, 'O'. 26-30, 'A'; Matanabe, K.; Megmann, T.G.; Tamaoxi, T.
J. Biol. Chem. 260, 5655-5660, 1985
A; Title: The human alpha-fetoprotein gene. Sequence organization and the 5' flanking reg
A; Reference number: A92520, MUID: 85192629; PMID: 2580830
A; Contents: annotation; gene, exons and introns
A; RAOyagi, Y.; Ikenaka, T.; Ichida, F.
A; Reference number: A93758; MUID: 79001617; PMID: 82265
A; Contents: annotation; metal binding
A; RAOyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res: 39, 3571-3574, 1979
A; Contents: Approprotein as a carrier protein in plasma and its bilitubin-binding abil A; Reference number: A90759; MUID: 8000170; PMID: 89900
A; Contents: annotation; bilitubin binding
A; Reference number: A90759; MUID: 80001710; PMID: 89900
A; Contents: annotation; bilitubin binding
A; Contents: Annotation; bilitubin binding
A; Contents: Annotation; bilitubin binding
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A,Map position: 4911-4913
A,Map position: 4911-4913
C,Map position: 4911-4913
C,Superfamily: 46/2; 90/3; 16/2; 205/3; 238/2; 238/2; 353/2; 397/3; 430/2; 476/3; 551
C,Superfamily: serum albumin: serum albumin repeat homology
C,Keywords: embryo: fetus; globulin; glycoprotein: metal binding: plasma
F;1-18/Domain: signal sequence alstatus experimental cxAT>
F;21-29/202/Domain: serum albumin repeat homology cSA1>
F;22-29/202/Domain: serum albumin repeat homology cSA2>
F;413-522/Domain: serum albumin repeat homology cSA2>
F;413-522/Domain: serum albumin repeat homology cSA2>
F;413-522/Domain: serum albumin repeat homology cSA2>
F;413-622/Domain: serum albumin repeat homology cSA3>
F;22/Binding site: copper (His) #status experimental
F;29/Binding site: bilirubin (Lys) #status predicted
F;25/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 'S',20-30,'A',32-37,'A' <AOY>
R;Ruoslahti, E.; Pihko, H.; Vaheri, A.; Seppala, M.; Virolainen, M.; Konttinen, A.
Johns Hopkins Med. J. Suppl. 3, 249-255, 1974
A;Title: 20. Alpha feroprotein: structure and expression in man and inbred mouse strains
A;Reference number: A93042; MJID:75018719; PMID:4138095
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Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>
Yachnin, S.; Hsu, R.; Heinrikson, R.L.; Miller, J.S.
iochim. Biophys. Acta 493, 418-428, 19-78.
Titchim. Biophys. Acta 493, 418-428, 19-73;11e: Studies on human alpha fectoprotein, Isolation and characterization of Reference number: A90624; MUD:77242506; PMID:70228
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A,Molecule type: protein
A,Residues: 'S',20-22,'S',24-35 <YAC>
A,Note: dimeric and imeric forms have been found in addition to the month of the forms and interior of the forms and interior of the month of the forms and interior and interior and interior forms and interior forms and interior forms and interior forms from interior forms and interior forms and interior forms from interior f
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Best Local Similarity 39.9%; Pred. No. 3.8e-75;
Matches 235; Conservative 116; Mismatches 231; Indels
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F;32-201/Domain: serum albumin repeat homology <SA1>
F;220-393/Domain: serum albumin repeat homology <SA2>
F;422-591/Domain: serum albumin repeat homology <SA3>
F;30/Binding site: copper (His) #status predicted
F;30/Binding site: copper (His) #status predicted
F;80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-
F;256/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 SQPITEFTEDPHVCEKYAENNEVFLGRYLHAVSRKHQELSEQFLLQSAKEYESLLNKCCK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 LVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLV 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 JIGIAHQMADIGEHCCAVPENQRWPCAEGDLTILIGKKCERQKKTFINNHVAHCCTDSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 DKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLCHKODNPNLPRLVRPEVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 EKPVGTLFFOKTCADPAVGVNYEWSKECCAKQDPERAQCFKAHRDHEHT --- SIKPEPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 MCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 DELRDEGKASSAKORIKCASLQKFGERAFKAWAVARLSCRFPKAEFAEVSKLVTDLTKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 KOLMKOSHSIEDKOHHFCWILDNFPEKVLKALNLARVSHRYPKAEFKLAHNFTEEVTHFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 KOCCHODMFECMTERLELTEHTCQHKDELSSKLEKCCNIPLJERTYCIVTJENDOVPAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSIAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRIAKTYETTLEKCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 AADPHECYAKVFDEFKPLVEEPQNLIKQNCELFECLGEYKFCNALLVRYTKKVPQVSTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 TDNPPSCYKDGADRFMNEAKERPAYLKQNCDILHEHGEYLFENSLLIRYTKKMPQVSDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 NRRPCFSALEVDETYVPKBFNAETFTFHADICTLSEKERQIKKOTALVELVKHKPKATKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 GMRSCFTALGPDEDYVPPPVTDDTFHFDDKICTANDKEKQHIKQKFLVKLIKVSPKLEKN
                                                                                                                                                                                                                                                                                                                                                                                                                            HKSEVAHRFKDIGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 HHKHIADVYTALTERTFKGLTLAIVSQNLQKCSLEELSKLVNEINDFAKSCINDKTPE-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 TCKLIKEHPDDLLSAFIHEBARNHPDLYPPAVLALTKQYHKLAEHCCBBBDKEKCFSBKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TECCHGDLLECADDRADLAXYI CENQDS I SSKLKECCEKPLLEKSHCI AEVENDEMPADL
                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                  Query Match 38.8%; Score 1205; DB 1; Best Local Similarity 39.3%; Pred. No. 3.3e-72; Matches 227; Conservative 108; Mismatches 239;
                  F;25-607/Product: 74K serum albumin #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 QLKAVMODFAAFVEKCCKADDKETCFAEEGKKLVAASQ
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(Species: Xenopus laevis (African clawed frog)
(Species: Xenopus) laevis (African clawed frog)
(Species: 31-Dec-1993 Haequence revision 31-Dec-1993 Hiext_change 22-Jun-1999
(SAccession: B41682; SO2693; Ā05288
(SAccession: B41682; SO2693; Ā05288
(SAccession: B41682; SO2693; Ā05288
(MOSKALIS, C.E., Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schoenberg, D.R.
MOS. Endocrinol: 3, 464-473, 1989
(A;Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic ad
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A:Residues: 1-48 <SCHS
A:Residues: 1-48 <SCHS
A:Residues: 1-48 <SCHS
Molffe, A.P.; Glover, C.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, C.L.; Tata, Eur. J. Blochem. 146, 489-496, 1985
A:Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and destabilizat A:Reference number: A05288; MUID:86126974; PMID:3971961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Accession: A05888
A,Molecule type: mRNA
A.Residues: 459-502, TL',504-557 <WOL>
A.Kolesidues: 459-502, TL',504-557 <WOL>
A.Cross-references: GB:M28276
A.Cross-references: GB:M28276
C.Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copponent: Serum albumin is synthesized in the liver as preproalbumin. It binds copponents with these hormones promote their transfer across the membranes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476
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                                                                                                                                                                                                                                                     DLIKVHTECCHGDLLBCADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVEND 296
                                                                                                                                                                                                                                                                                                                                                                                        EMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLURLAKTYETT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEKCCAAADPHECYAKVFJEFKPLVEEPQNLIKQNOELFEQLGEYKFQNAJLVRYTKKVP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEKCFOTENPLECODKGEEELOKYIQESOALAKRSCGLFOKLGEYYLCNAFLVAYTKKAP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHK 536
                                                                                                                                                                                                                                                                                                                   DVAHVHEHCCRGDVLDCLQDGEKIMSYICSQQDTLSNKITECCKLTTLERGQCIIHAEND 320
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VEPVTSCEAYESDRETFMNKPIYEIARRHPFLYAPTILLMAARYSXIIPSCCKAENAVE
                                                                                                                CLLPKLDELROEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRPPKAEFAEVSKLVT
                                                                                                                                                                                 CFQTKAATVTKELRESSLINQHACAVMKNFGTRTFQAITVTKISQKFTKVNFTEIQKLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLISSELMAITRKWAATAATCCCLSEDKLLACSEGAADIIIGHLCIRHEMTPVNPGVGQC
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A;Reference number: A41682; WUID:93313788; PMID:2747653
A;Accession: B41682
A;Accession: B41682
A;Mcdecule type: mRNA
A;Residues: 3.607 < MOS.
A;Chotopp, M.; Doebbeling, U.; Wagner, U.; Ryffel, G.U.
5. Mol. Biol. 199, 83-93; 1988
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242 265 302 325 362

122 145 182 205

52 88

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422 445 542

565

Keywords: carrier protein, duplication, glycoprotein, metal binding, plasma 1-18/Domain: signal sequence #status predicted <SIG>

F:19-24/Domain: propeptide #status predicted <PRO>

Superfamily: serum albumin; serum albumin repeat homology

Genetics

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SEQUENCE FROM N.A.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9666,
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MEDINE=82381882, PubMed=6171778,
Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,
Najarian R.C., Seeburg P.H., Wion K.L.;
The sequence of human serum albumin cDNA and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (FROSD03/PROI708/PRO2044/PRO2619/FRO2675). TISSUE=Fetal liver;
Zharg C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;
"Functional prediction of the coding sequences of 121 new genes deduced by analysis of CDNA clones from human fetal liver.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=86196112; PubMed=3009475;
Mingretti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Ha Beattie W.G., Dugaiczyk A.,
"Xolecular structure of the human albumin gene is revealed nucleotide sequence within q11-22 of chromosome 4.";
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PRT; 609 AA.
P02768; 095574; Q13140; Q92157; Q9P117; Q9UHS3; Q9UJZC; 2: JUL-1986 (Rel. C1, Created)
0: APR-1990 (Rel. 14, Last sequence update)
15-SP-2003 (Rel. 42, Last annotation update)
Serum albumin precursor.
ALB.
Eukaryore: Manan).
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-82105994; Pubmed-6275391;
Dugaiczyk A., Law S.W., Dennison O.E.;
Nucleotide sequence and the encoded amino acids
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              TISSUBLIVER, and Skeletal muscle;

WEDLINE=22388257; PubMed=12477932;

Attausherg R.L., Feingold E.A., Grouse L.H., Derge C.G.,

Ratausherg R.L., Teingold E.A., Grouse L.H., Derge C.G.,

Attschul S.F., Zeeberg B., Magner L., Sheamen C.M., Schuler G.D.,

Attschul S.F., Zeeberg B., Mactow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,

And Stapleton M., Soares M.B., Bondido M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., NcKernan K.J., Malek J.A., Gunarathe P.H.,

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A Notlaion D.K., Muany D.M., Scdergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Cheneration and initial analysis of more than 15,000 full-length
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MEDLINE=86140099; PubMed=2419329;
Uranc Y., Watchnabe K., Sakai M., Tamacki T.;
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Teleman 261:3244-3251(1986).
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Biochem. J. 171:453-459(1978).
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"Lysine residue 199 of human serum albumin is modified by
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"Disulfide bonds in human serum albumin.";
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(In) Bing D.H. (eds.);
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SEQUENCE OF 222-229.
MEDLINE=76257808; PubMed=955075;
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MEDLINE=78186630; PubMed=656055;
Jacobsen C.;
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FEBS Lett. 66:173-175(1976).
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MEDLINE=92190239; PubMed=1347703;
Mirchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
Rochu D., Porta F.;
"Two alloalbumins with identical electrophoretic mobility are produced
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Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
Walkins S., Putnam F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION OF VARIANT REDHILL.
MEDLINE=90115852; PubMed=2164980;
Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;
A.Lbumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of human serum albumin whose precursor has an aberrant signal peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS 10MA CITY-2 VAL-25; 10MA CITY-1 VAL-389; KONAGOME-3 HIS-23; KONAGOME-1 AND KONAGOME-1 GIU-396.

KONAGOME-2 AND KONAGOME-1 GIU-396.

MAEDINE-92052189; PubMedi-1946412.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90115905; PubMed=2404284;
Arai K., Madison J., Shamuzu A., Putnam F.W.;
"Point substitutions in albumin genetic variants from Asia ";
Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
                                                                                                                                                                                                                                                                                    VARIANTS NAG-2 AND NAG-3.
MEDLINE-88068523; Pubmed-3479777;
Takkhashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
Satof C., Neel J.V.
"Amino acid substitutions in inherited albumin variants from
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A doroz spiice mutation and a single-base deletion produce carboxy:-terminats of imman serum albumin.";
Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
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Proc. Natl. Acad. Sci. U.S.A. 84:8031-8005(1987).
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Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989)
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MEDLINE=91296740; PubMed=2068071;
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                                   MEDLINE=87157744; PubMed=3828358; Brennan S.O., Herbert P.;
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JARIANT CANTERBURY ASN-337.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ALBUMIN 2.
ALBUMIN 3.
COPPER (BY SIMILARITY).
BY SIMILARITY.
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               -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY -!- SIMILARITY: Contains 3 albumin domains.
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HSSP: P02768; 1E78
Interport : PR000264; Serum_albumin.
PERINTS: PR000273; transport_prot: 3.
PRINTS: PR00002; SERUMALBUMIN.
PR000715; PR00012; ALBUMIN; 3.
PR0071E; PS00212; ALBUMIN; 3.
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-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELJULAR LOCATION: Secreted.
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Mammalla, Eutheria, Primates, Catarrhini, Cercopithecidae,
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               tch 100.0%; Score 3103; DB 1; Lergth 609; al Simitarity 100.0%; Pred. No. 1.7e-194; 585; Conservative 0; Mismatches 0; Indels 0
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Pred. No. 2.4e-159;
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I -> T (IN REF. 2).

S -> A (IN REF. 1).

V -> V (IN REF. 1).

D -> E (IN REF. 1).

3 GFICE F7 DDB FCO GRC
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                                                          SERUM ALBUMIN.
ALBUMIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Allergy Clin. Immunol. 93:614-627(1994).

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. (a(2+), Na(+), K(+), fatty acids, hormones. billirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELULIAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
-!- SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 25-48.
MEDLINE=75011422; PubMed=4414513;
Dixon J.W., Sarkar B.;
"Isolation, amino acid sequence and copper(II) binding properties of peptide (1-24) of dog serum albumin.";
J. Biol. Chem. 249:5872-5877(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
              Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn M.J., Corbett J.M., Wheeler C.H., "HSC-2DPAGE and the two-dimensional gel electrophoresis database dog heart proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Salivary gland;
MEDLINE-94201492; pland;
Spitzauer S., Schweiger C., Sperr M.R., Pandjaltan B., Valent P.,
Muehl S., Ebner C., Scheiner C., Kraft D., Rumpold H.;
"Molecular characterization of dog albumin as a cross-reactive allergen."
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=201448667; PubMed=10669848;
Pandjaitan B., Swoboda I., Brandejsky-Pichler F., Rumpold H.,
Valenta R., Spitzauer B.
"Esplerichia coli expression and purification of recombinant dog
albumin, a cross-reactive animal allergen.";
J. Allergy Clin. Immunol. 105:279-285(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SK03103; ALBUMIN; 3.
PROSITE; PS0212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
                                                                                                                                                                                                                      STRAIN=Beagle; TISSUE=Liver;
Higer C.,
Submitted (MAR-1999) to the EMBL/GenBank/DDEC databases.
Serum albumin precursor (Allergen Can £ 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSC-2DPAGE; P49822; DCG.
InterPro; IPR000264; Serum_albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ectrophoresis 18:2795-2802(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98163340; PubMed=9504812;
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLDELRDEGKASSAKQRLKCASLCKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK 240
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                                                                                                                                                                                                                                                                                                                                                                                 25 DTHKSEIAHRFNDLGEKHFKGLVLVAFSQYLQQCFFEDHVKLVNEVTEFAKKCAADESAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNAJLVRYTKKVPQVST
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                             79.8%; Score 2475.5; DB 1; Length 607; 76.3%; Pred. No. 9.8e-154; Live 69; Mismatches 68; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583
                                                                                                                                                       68598 MW; 256F6E830A1B90C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 KEQLKTVLGNFSAFVAKCGREDKEACFAEEGPKLVASSQLAL
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SEQUENCE FROM N.A., AND VARIANT THR-214.
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Best Local Similarity 76.3%
Marches 445; Conservative
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MEDINE-9345495; PubMed=8344282;

MEDINE-9345495; PubMed=834682;

MEDINE-9346495; PubMed=834682;

MEDINE-9346495; PubMed=834682;

MEDINE-9464982; PubMed=834682;

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MEDINE-9464982; PubMed=834682;

MEDINE-9464982;

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Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
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ALBUMIN 3.
COPPER (BY SIMILARITY).
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; PR050264; Serum_albumin.
Pfam; PF00273; Yaansport_Drot; 3.
PR1MTS; PF00273; Yaansport_Drot; 3.
PRODom; PE002486; Serum_albumin; 1.
SWART; SW00.03; KLBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 3.
PROFEP 19 24 SIMILA PROPEP 19 24 SIMILA CHAIN 25 607 SERUM ALB DOWAIN 25 204 ALBUMIN; 25 DOWAIN 21 396
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EMBL, X58999; CAA41735.1; -.
EMBL, Y17769; CAA76847.1; -.
EMBL, AF542068; AAN17824.1; -.
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MCGILINE=80024273; PubMed=488139;
MCGILIIvray R.T.A., Chung D.W., Davie E.W.;
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                                                                    SEQUENCE FROM N.A., AND VARIANT THR-214.
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                              SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214 Brown J.R.;
                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
[10]
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                                                                                                                                                                                                                                     Brown J.R.;
Submitted (APR-1975) to the PIR data bank
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Fed. Proc. 34:591-591(1975).
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                                                                                                                                                                                                                          REVISIONS TO 190-195
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N -> D (IN REF. 6).
ST -> TS (IN REF. 6).
K -> R (IN REF. 12).
SE -> ES (IN REF. 6).
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71; Mismatches 69;
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                                                                                                                                                                 DIPSILAADEVESKDVCKNYAEAKDVFLGMFI/VEYARRHPDYSVVLILLRIAKTYETTLEKC 360
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                                                      VHTECCHGDJJECADDRADJAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                      CAAADPHECYAKVFDEFKPIVEEPQNIIKQNCELFEQIGEYKFQNALLVRYTKKVPQVST 420
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Mammalia, Eutheria, Lagomorpha, Leporidae, Cryctolagus.
NCBI_TaxID=9986;
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PERM, PF00273; transport prot; 3.

PRINTS; PR000020; SERVIMALBUXIN.

SMART; SM00103; ALBUMIN.

PROSITE; PS00212; ALBUMIN.

Metal-binding; Lipid-binding; Repeat; Signal; Copper.

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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor.
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Oryctolagus cuniculus (Rabbit).
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2 CRC64;	; Length 608; 2; Indels 0; Gaps 0;	DHVKLVNEVTEFAKTOVADESAE 60 	PERNECFLQHKDDNPNLFRLVRPEV 120	AKRYKAAFTECCGAADKAACLLP 180 - - 	RLSQRFPKAEFAEVSKLVTDLTK 240 	CCEKPLLEKSHCIAEVENDEMPA 300	HEDYSVVLLERLAKTYETTLEKG 360 	OLGEYKFONALLVRYTKKVPQVS: 420 :	SVV.NQLCVLHEKTPVSDRVTKCCTES 480	EKERQIKKÇTALVELVKHKPKAT 540 	ASOAALG 584 : - - - - -	
SERUM ALBUMIN. ALBUMIN 1. ALBUMIN 2. ALBUMIN 3. COPPER. BY SIMILARITY.	8%; Score 2446; DB 1 1%; Pred. No. 8.1e-15 77; Mismatches 7	BENFKALVLIAFAQYLQQPPFEDHVKLVNEVT 	GEMADCCAKÇE 	OVMCTAFHDNEETFLKKYLYBIARRHPYFYAPBLLFFAKRY : : OVLCKAFHDDEKAFFGHYLYBVARRHPYFYAPBLLYYAQKY	SSAKQRLKCASLQKFGERAFKAWAVARI 	CADDRADLAKYICENQDS.ISSKLKEC 	FVESKDVCKNYAEAKDVFLGMPLYEYARRHPDVS 	KPLVEEPQNLIKQNCELFE : OPLVDEPKNLVKQNCELYE	CCKHPBAKRMPCAEDYL: 	TYVPKEFNAETFTFHADICTLS 	EKCCKADDKETCFAEEGKKJVA :	: PRT; 607 AA.
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                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostoni,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.4%; Score 2432.5; DB 1; Length 607; 75.0%; Pred. No. 6.1e-151; Live 73; Mismatches 72; Indels 1;
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seguence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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HSSP: PC2768; 1278.
INDERPO: IRROGOS4; Serum_albumin.
PF00273; transport prot: 3.
PRINTS: PR00802; SERUMIABUMIN.
PRODOM: PD002486; Serum albumin; 1.
SYART; SW00103; ALBUMIN; 3.
PROSITE: PS00212; ALBUMIN; 3.
Metal-binding; Lipideiding; Repeat; SIGNAL.
                                                                                                                         MEDLINE=90098888; PubMed=2602160;
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437; Conservative
                                                               Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
NCBL TaxID=9940;
                             Serum albumin precursor
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                                       84
JAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAE
                        NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV
                                                                                                                                                                                                     144 DILCAEFKADEKKFWGKYLYBVARRHPYFYAPELLYYANKYNGVFOECCOAEDKGACLLP
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21-JUL-1986 [Rel. 01, Last sequence update)
23-FEB-2003 (Rel. 41, Last annotation update)
Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)]
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Mammalia, Sutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
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MEDLINE=81223722; PubMed=7017712;
Sargent T.D., Yang M., Bonner J.;
"Nucleotide sequence of cloned rat serum albumin messenger RNA.";
Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
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MEDLINE=77249657; PubMed=893447;
Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts is traves A.W., Per-proablumin: complete amino acid sequence of the piece. Analysis of the direct translation product of albumin
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MEDLINE=78109429; PubMed=564345;
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AC P02770; P11382;
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SEQUENCE OF 166-174.
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DVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLP 180
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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                                                                                                                                                                                                                                                                                 Length 608;
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Baldwin G.S., Weinstock J.;
"Nucleotide sequence of porcine liver albumin.";
                                                                                                                                                                                                                                                                                 78.2%; Score 2426; DB 1; 73.4%; Pred. No. 1.6e-150;
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1D ALBU_PIG

AC P08835, Q23018,

D1 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                              al Similarity 73.43
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VARIANT
CONFLICT
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MEDLINE=79001617; PubMed=80265;
Apyagi Y., Ikenaka T., Ichida F.;
Apyagi Y., Ikenaka T., Ichida F.;
Copper (II)-binding ability of human alpha-fetoprotein.";
Cancer Res. 38:3483-3486(1978).
Cancer Res. 38:3481-3486(1978).
Cancer Res. 38:3481-3486(1978).
Cancer Res. 38:3481-3486(1978).
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                                                                                                                                                                                                                     and
                                                                                                               SECUENCE OF 223-288 AND 572-608.
MEDLINE=76260153; PubMed=956149;
Isemura S., Ikenaka T.;
Fragmentation of rat serum albumin by cyanogen bromide cleavage.
the amino acid sequences of four fragments.";
J. Biochem. 79:1183-1196(1976).
acid sequences of fragments I and II obtained by cyanogen
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Plasma;
MEDLINE=87194805; PubMed=243711:;
Carraway R.E., Mitra S.P., Cochrane D.E.;
"Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(s).";
J. Biol. Chem. 262:5968-5973(1987).
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HSSP; P02768; IESP.
Interpro; IPSC000564; Serum_albumin.
Pfam; PF00273; transport_pro; 3.
PRINTS; PR00802; SERUMALBUMIN.
Proport P002466; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSTTE; PS00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
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NEUROTENSIN-RELATED
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                            bromide cleavage of rat serum albumin.
J. Biochem. 83:35-48(1978).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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           KLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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PIR; JCS838; JC5838.
HSSP, P02768; LESP.
INCEPTO; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
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NCBI_TaxID=10047;
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Nucleic Acids Res. 16:9045-9045(1988).

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water. (a(2+), Na(+), K(+), fatty acids, binding capacity for water. (a(2+), Na(+), K(+), fatty acids, hormones, bilitubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-:- SUBCELLUIAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
-:- SIMILARITY: Contains 3 albumin domains.
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EMBL, M3647, AAA30980.1;
PIR, S01332, AABOG.
HSSP, PO2768; LFTH
InterPro, IPRC0264; Serum albumin,
Pfam, PF00273, transport proc;
PRINTS; PRC0802; SERUALBUMIN,
Probon, PD0C2486; Serum albumin,
SMART; SM00703; ALBUMIN, 3.
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Azakawa T., Hara A., Ehbbara K., Yoshino M., Itoh M., Ishii y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azitawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Kuehi B., Lewis S., Matsud Y., Nikali B., Kochiwa H., Kuehi P., Lewis S., Matsud Y., Nikali R., Tomita M., Wagner L., Washio T., Saki K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Bottincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchinoni L., Mashima M., Marking M., Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wayashizaki Y.,
F., Functional annotation of a full-length mouse cDNA collection.";
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"Mouse liver protein database: a catalog of proteins detected by two-dimensional gel electrophoresis.";

Electrophoresis 13:970-99. [1992.]

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELLULAR LOCATION: Secreted.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
         567 EQLKKVMGDFAEFLEKCCKQEDKEACPSTEGPKLVAESQKAL 608
                                                                                                                                                    ALBU MOUSE STANDARD; PRT; 608 AA. 02.724; Q61802; C1-AB. 07. Created) 15-JUL-1999 (Rel. 38, Last sequence update) 28-PEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE-21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                      Serum albumin precursor.
ALB OR ALB1 OR ALB-1.
Mus musculus (Mouse).
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ALBUMIN 3.
PRINTS, PROC802; SERUMALBUMIN.
PRODOM, PSO02486. Serum albumin; SMART, SX00103; ALBUMIN. PROSITE; PSO0212; ALBUMIN; 3.
                                                                                                                  Metal-binding, Lipid-binding,
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Blophys. Res. Commun. 78:1060-1066(1977).

-!- FUNCTION: Serum albumin, the main protein of plasma, has a good birding capacity for water. Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
-!- SIMILARITY: Contains 3 albumin domains.
                                                  VHTECCHGDILECADDRADLAKYICENQDSISSKIKECCEKPLLEKSHCIAEVENDEMPA
                                                                                                               DLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPJYSVVLLLBLAKTYETTLEKC
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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EMBL/GenBank/DDBJ databases.
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01-NOV-1990 (Rel. 16, Created)
01-NJG-1992 (Rel. 23, Last sequence update)
28-FPB-2003 (Rel. 41, Last annotation update)
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J. Biol. Chem. 258:4556-4564(1983).
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MEDLINE=78019943; PubMed=911327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cassady A.I., Salklid C.K.,
Submitted (JJL-1991) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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SMART; SM00103; ALBUXIN; 3.
PROSITE; PS00212; ALBUXIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
SIGNAL
TISSUE SPECIFICITY: Plasma.
SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
SIMILARITY: Contains 3 albumin domains.
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I (IN REF. 5).
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Pred. No. 2.1e-147;
80; Mismatches 91;
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InterPro; IPR060264; Serum albumin.
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                                                                                                                                                                                         EMBL; AJ011413; CAA09617.1; -.
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EMBL; X13060; CAA31458.1; -.
EMBL; AX010025; BAB26650.1; -
                                                                                                                                                                                                                                                  PIR; A35139; A05139.
HSSP; P02768; 1E7B.
SWISS-2DPAGE; P37724; MOUSE.
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PIR; JC4258; JC4258.
HSSP, D02768; IEPB.
InterPro; IPR000264; Serum_albumin.
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PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SMC0103; ALBUMIN; 3.
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        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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118; Mismatches 192; Indels
                                                                                     EMBL: X60688; CAA43098.1; -
EMBL: V00381; CAA23680.1; -
PIR; S15571; ACAES.
HSSP: P02768, BETB.
InterPro: IPR00264; Serum_albumin.
Pfam; PP0273; transport_prot; 3.
PR.INTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SM00212; ALBUMIN; 3.
PRCSITE; PR00212; ALBUMIN; 3.
PRCSITE; PR00212; ALBUMIN; 3.
PRCSITE; PR00212; ALBUMIN; 3.
Metal-binding; Lipid-binding; Repeat; Signal; Copper.
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ALBUMIN 2.
European Bioinformatics Institute.
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273; Conservative
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                                                                                                                                                                                                                          390 KIDNPAECYANAQEQLNQHIKETQDVVKTNCDLLHDHGEADFLKSILIRYIKKMPQVPTD 449
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Gene 152:213-220(1995).
Gene 153:213-220(1995).
Gene 153:213-220(1995)
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Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel;
Signal.
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8-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update;
Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan
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-!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
-!- SIMILARITY: Contains 3 albumin domains.
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SEQUENCE OF 1-28 FROM N.A.
MEDILTB-921-87885, PubXed=7684942;
MEDILTB-921-87885, PubXed=7684942;
Tilghman S., Krumlauf R., Tuddenham E.G.D.:
"A G.->A substitution in an HNF I binding site in the human alpha-
feroprorein gene is associated with hereditary persistence of alpha-
fetoprotein (HPAFP).":
                                                                                                                                                      Morinaga T., Sakai M., Wegmann T.G., Tamaoki T.;
"Primary structures of human alpha-fetoprotein and its mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 80:4604-4608(1983).
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87185438; PubMed=2436661;
Gibbs P.E.M., Zielinski R., Boyd C., Dugaiczyk A.;
Gibbs P.E.W., alelinski R., Boyd C., Dugaiczyk A.;
Structure, polymorphism, and novel repeated DNA elements a complete sequence of the human alpha-fetoprotein gene.";
Biochemistry 26:1332-1343(1987).
   lpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-
                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=83273664; PubMed=6192439;
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MEDLINE=91242409; PubMed=1709810;
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MEDLINE=78001760; PubMed=71198;
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                                                 sapiens (Human)
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Tamaoki T., 
"The human alpha-fetoprotein gene. Sequence organization and
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Ceccarini C., Terrana B.;
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                                                                                                                                                                                                                                                                                C. Natl. Acad. Sci. U.S.A. 82:7160-7164 (1985).
FUNCTION: BINDS COPPER, NICKEL, AND FATTY ACIDS AS WELL AS, AND STIRRUEN LESS WELL THAN, SERUM ALBUMIN. CNLY A SMALL PERCENCAGE (LESS THAN 2%) OF THE HUMAN AFP SHOWS ESTROGEN-BINDING PROPERTIES. SUBUNIT: DIMERIC AND TRIMERIC FORMS HAVE BEEN FOUND IN ADDITION TO THE MONOMERIC FORM.
                                                                                                                                  MEDLINE=80001710; PubMed=89900;
Aoyagi Y., Ichaaka T., Ichida F.;
Alpha-Petoprotein as a carrier protein in plasma and its bilirubin-
binding ability.";
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: PLASMA. SYNTHESIZED BY THE FETAL LIVER AND
YOLK SAC.
                                                                                                                                                                                                                                 MEDLINE=86042625; PubMed=2414772;
Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
"Tyrosine sulfation of proteins from the human hepatoma cell line
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Pfam; PF00273; transport pro; 3.
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PRODOM: PR002486; SERUMALBUMIN; 1.
SWART: SW0103; ALBUMIN; 2.
PROSITE: PS00212; ALBUMIN; 2.
Glycoprotein; Sulfation; Repeat; Metal-binding; Copper; Nickel; Signal; Polymorphism.
                                                               Aoyagi Y., Ikenaka T., Ichida F.,
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Cancer Res. 38:3483-3486(1978).
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Chem. 260:5055-5060(1985)
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EMBL, M10950, AAA51675.1; --
EMBL, W10514, CAA24758.1; --
EMBL, M16110, AA58754.1; --
EMBL, Z19532, CAA79592.1; --
EMBL, A26524, FPHJ.
HSSP, PC2768, 1875.
Glycosuite98, P02771; --
Siena-2DFAGE; P02771; --
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Best Local Similarity 39.9%; Pred. No. 4.4e-74;
Matches 235; Conservative 116; Mismatches 231; Indels
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/FTIG=CAR 000070.
-> G (in dbSNP:1057173).
/FTIG=VAR 012049.
ALBUMIN 3.
COPPER AND NICKEL.
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61 NCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                    1 DAHKSEVAHRFKDLGEENFK......TCFAEEGKKLVAASQAALGL
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Q8MJ06
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Perfect score:
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1 C8R0J9 1 090K51 1 091X31 1 091X31 1 091X31 3 090WZ8 3 090WZ8 3 090WZ8 6 09ZLV0 6 0	PRT; 608 , Created) , Last sequence, Last sequence, Last annotation sommaridae; Sch. Scomaridae; Sch. Lover its a novel T. Lower its annotation in the season in the seaso	HFKGLVLIAFS
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                                                                 VHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPA 300
                                                                                                                                   DIPSIAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVILLRLAKTYETTLEKC 360
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                   205 KLDGVKEKALVSSVRQRMKCSSMQKFGERAFKAWAVARLSQTFPNADFAEITKLATDLTK 264
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                                                                                                                                                   PILVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18: ALVSSVRQRMKCSSMQKFGERAFKAMAVARLSQTFPNADFAEITKLATDLTKVNKECCHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNEETFLKKYLYETARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKASSAKORLKCASLOKFGERAFKAMAVARLSORFPKAEFAEVSKLVTDLTKVHTECCHG
KLJELRJEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 HRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/60; TISSUE=Thymus;
MBDLNE=2354683; PubMed=1246681;
The FANTOM Consortium,
The FANTOM Consortium,
The FANTOM Consortium,
The FANTOM Consortium,
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Wature 420:563-573(2002)
EMBL; AKCS0644; BAC34360.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                           54: KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583
                                                                                                                                                                                                                                                                                                                                                                                                                               565 AEQLKTVMDDFAQFLDTCCKAAACKOTCFSTEGPNLVTRCKDTL 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Best Local Similarity 72.2
Matches 415; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                           PILVEVSRNIGKVGSKCCKHPEAKRNPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES 480
DVMCTAFHDNEETFLKKYLYBIARRHPYFYAPBILFFAKRYKAAFTECCQAAJKAACLIF 180
                   :45 EAMCTSFQENAVTFMGHYLHEVARRHPYFYAPELLYYAEKYSAIMTECCGEADKAACITP 204
                                                                 240
                                                                                                  KIDALKEKALASSVNÇRIKCSSLQRFGQRAFKAWAVARMSQKFPKADFAEITKLATDLTK 254
                                                                                                                                  241 VHTECCHGOLLECADDRADLAKYICENQOSISSKLKECCBKPLLBKSHCIAEVBNDEMPA 300
                                                                                                                                                       DLPSJAADFVESKDVCKNYAEAKOVFJGMFLYEYARRHFDYSVVLLLRLAKTYETTLEKG 360
                                                                                                                                                                                                                                       384
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STRAIN-GSTBL/60; TISSUE-LIVEY;
MEDLINE-CSTBL/61; TISSUE-LIVEY;
MEDLINE-2234683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Marure 426:563-573(2002).
MBL; AKUSCO448; BAC34145.1;
FMBL; AKUSCO448; BAC34145.1;
FMBL; AKUSCO448; BAC34145.1;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 GPQLRIVLGEFTAFLDKCCKAEDKEACFSEDGPKLVASSQAAL
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421; Conservative
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Mus musculus (Mouse)
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Best Local S:
Matches 421,
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| CAAADPHECYAKVFDEFRPLVEEPQNLIKQNCELFEQLGEYKFQNALJVRYTKKVPQVST 420
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                                          CAAADPHECYAKVEDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVST
                                                                                                                                                                PILVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNOLCVLHEKTPVSDRVTKCCTES
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      CAAAADPHECYAKVEDEFKPLVEEPQNLIKQNCELFEQLSEYKFQNALLVRYTKKVPQVST
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Sphenodontia, Sphenodontidae, Sphenodon.
VCBI_TaxID=8508;
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Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;

Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;

Partial coding sequence for Sphenodon punctatus 68 kDa alb
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF375971; AAM46104..;

InterPro. IPR00204; Serum albumin.

PRODOM; PR00273; Lransport prot; 3.

PRINTS; PR00216, Serum albumin; 1.

PRODOM; PD002486; Serum albumin; 1.

SMART; SMO0103; ALBUMIN; 3.

PROSITE; PS00212; ALBUMIN; 3.
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                                                                                                                                                                                                                                                                                                                                                                                 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
                                                                                                                                                                                                                                                                                                                                                                                                                    527 AA; 59711 MW; C62B799E387F5929 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Serum albumin (Fragment)
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Best Local Similarity 45.9°
Matches 240; Conservative
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SEQUENCE
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DLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLFSLAAD 308
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                                                                                                                                                                                                                                                 CYAKVFDEFKPLVEEPQNLIKONCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSR
                                                                                                                                                                                                                                                                                     SALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVM
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                                                                                                                        FVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHE
                                                                                                                                                                                                                                                                                                                                                                             NLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCF
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eureleostomi.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 213;
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Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDSJ databases
EMBL; EC03S969; AAH35969.1;
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11-MR-2003 (TrEMBLrel. 23, Created)
01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to serum albumin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.1%; Score 1865.5; DB 4 63.6%; Pred. No. 1.6e-138; vative C; Mismatches O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOFAAFVEKCCKADDKETCFAEEGKKLVAASQAAL 583
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Matches 372; Conservative
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57 ESAENCDKSLHTUFGDKLCTVATURETYGEMADCCAKQEPERNECFLQHKDDN-PNLPRU 115
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                      GQCFNDKMPEHKQEVEYVCALQXHNCYILQDFKERALTAYKAVQASQKFPLASFENVQII 267
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 SKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVD 494
                                                                     ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAF 554
                                                                                               176 A-CLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 VRPAPEQICKDHAENRGPLLARYIFMLAIGHPHMYIPAILGFAQRFDGIVSHCCKDVBTA
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                                                                                                                                                                                                                                                                                                                                                                                                             Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B., "Serum albumin of the mole salamanders Ambystoma maculatum Ambystoma texanum.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF21183; AAL56646.1; -.
InterPro; IPR000264; Serum albumin, Pfam; PF00023; transport, prot; 3.
Prints; PR00802; Serum albumin, Prints; PR00802; Serum albumin, SMRTT; SM00103; ALBUMIN; 3.
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SERUM ALBUMIN.
9D66F57F174AC23F CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                              555 VEKCCKADDKETCFAEEGKKLVAASQAALGL 585
                                                                                                                                                                                                                                                                   626
                                                                                                                                                                                                                                                                                                                                                                                              Ambystoma maculatum (spotted salamander)
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626
70677 XW;
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01-M4R-2002 (TrEMBLrel. 20,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           Serum albumin precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRJAKTYETTLEKCCAAADPHECYAKVF 374
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 480
                                                                   LVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKAT 540
                                                                                               423 YALRSLCITSLGGDEKFVPIBFSADLFTFHEDJCHAAQDKLGERKQQMIVNLVXHKPNIT 482
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                        364 EELIFYTR-ITKAASRCCEVSVDKKLPCTEGYVDFVLGQICQRHQRSSINVNVCQCCSNS
421 PTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 EENFKALVLIAFAQYLQQCFFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLC
                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 1242; DB 6; Length 609; 40.5%; Pred. No. 2.7e-89; ive 113; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FULUICHI M., Nec S., Hisasue M., Tsuchiya R., Watanabe M., Hashizaki K., Hisanatsu S., Yamada T.;
Hashizaki K., Hisanatsu S., Yamada T.;
Canine alpha-feroprorein cDNA.",
Submitted (AUG-2002) to the EMBL/GerBank/DDBJ databases.
RMBL; AB089789; BAC07513.1;
Interpro. IPR000264; Serum albumin.
ProDom, PR00273; Ltansport prot. 3.
PRINTS; PR00802; SERUMALBÜMIN.
RPTODM; PR002486; Serum albumin; 1.
RPTODM; PR002486; Serum albumin; 1.
RMART; RN00103; ALBUMIN; 2.
SMART; RN00121; ALBUMIN; 2.
SEQUENCE 609 AA; 68782 MW; BE4B8250C5AF2AFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Canis.
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                                                                                                                                      541 KEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASCAAL 583
                                                                                                                                                            483 XEQLOTVFGGFTKMTEKCCKAEDHEACFGEEGPKLVAESQTAL 525
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
NCBL_TaxID=9615,
                                                                                                                                                                                                                                                                                                    Created)
Last sequence update;
Last annotation update)
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Best Local Similarity 40.5
Matches 231; Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog)
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                                                                                                                                                  GAACCHISEDRQLACGEGAADLIIGQLCIRHEEMPINPGVGCCTSSYANRRPCFSSLVL 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 LCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNP-NLPRLVRPEVDVMCTAFHDNEE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 ICKTPENPEKYPFHEGCCKKEDPERHKCFIEHKSTDPKERTEYVKPSPEGICKDHAENRD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 EFLGHYIHKVASSHTTMYPPAILSFTLHFDGIVSHCCKDEATVGQCLSEKMPAHKEEVEH 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 IGVEHAKALAMALFSQMLSKCPHHEQVQRVRNVMDIADLCSRGAKHGDCGKSVMTIILNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ambystoma texanum (Smallmouth salamander).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haverfield E.V., Uzzell T., Spolsky C.M., Bazartseren B., "Serm albumin of the mole salamanders Ambystoma maculatum Ambystoma texanum."
Submitted (DEC-1999) to the EMBL/GenBank/DD3J databases.
EMBL, AF217182, AALS6645.1, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Match 35.0%; Score 1087; DB-13; Length Local Similarity 37.7%; Pred. No. 4.38-77; les 214; Conservative 102; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERUM ALBUMIN.
DE08533BF4953EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                              554 FVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
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624
70321 MW,
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624 AA;
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NCBI_TaxID=8304;
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                                                                                                                                                                                                                                                                                                     508 QCCSHSLSSQTPCFSALPVDETYVPPPLSVASFNFNDELCTTSEPEQQSKKQVFLIRLMK 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 FDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g)
O)
                                                                   40 EMNLVDLATIFFAQFVQEATYKEVNQMVKDVLTVIEKSTGSEQPAGCLANQVSVFLEBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 TVATLRETYGEMADCCAKQEPERNECFLQHKDDNP-NLPRLVRPEVDVMCTAFHDNEETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 MTRYIYEIARRHPFLYAPTILSLAAQYDKIIPPCCKAENAVECFQTKAASITKELRESSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 KORLKCASLOKFGERAFKAWAVARLSORFPKAEFAEVSKLVTDLTKVHTECCHGDLLECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 LNQHMCTVMRQFGARTFRAITVTKLSQKFPKANFTEIQKLVLDVAHIHEECCRGNVLECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 QDAERVVSYVCSQQDTLSSKIAECCKLPTTLELGQCIIHAENDGKPEGLSPNLNRFLGER
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                        355 ITLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNGELFEQLGEYKFQNALLVRYTKK
                                                                                                                                            VPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVV1NQLCVLHEKTPVSDRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 EENFKALVIJAFAQYLQQCPFEDHVKLYNEVIEFAKTOVADESAENCDKSIHTLFGDKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                  535 HKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL 585
                                                                                                                                                                                                                                                                                                                                                                                                                          568 QYPHMTDEQLKTCVVNFVPMVDQCCKADNHNECFALEGAKLIDACKAILAV 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Kim J.G., Nonceman D., Vallet J.L., Christenson R.K.:

"Mapping of the porsine alpha-feroprotein (AFP; gene to SSCB.";

Submitted JUN-2002) to the EMBL/GenBank/JDBJ databases.

EMBL, AFS17770, AAM66710.1;

InterPro, IPR000264; Serum_albumin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0c273; transport prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
PR000m; PD002486; Serum albumin; 1.
SMART; SM00103; ALBUMIN; 2.
PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 610 AA; 68624 MW; C985BEAD44963D5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Greated)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last armotation update)
Alpha-fetoprotein.
Sus screta (Flg).
Enkaryote, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225;
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Best Local
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Matches
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395 BELGKHIEESQALSKQSCALYQTLGDYKLQNLFLIGYTRKAPQLTSAELIDLTGKMVSIA 454 435 SKCCKHPEAKRAPGAEDYLSVUNQLCVLHEKTPVSDRVTKCTTESLVNRRPCFSALEVD 494 55 SKCCKHPEAKRAPGAEDYLSVUNQLCVLHEKTPVSDRVTKCTTESLVNRRPCFSALEVD 494 55 STCCQLSEKAGCGEGMADIFICRINBASPVNSGISHCNSSYSNRALGITSFLRD 514 65 STCCQLSEKAGCGEGMADIFICRISKERROIKKOTALVELYKRAFKSDLKAMDDFAAF 554 515 ETYAPPRPSEDKFTFPHKDLCQAHGKALQTMKQELLINLVKQKPELTEEQLAAVTADFSGL 574 515 VEKCCKADKETCFAEGGKKLAASQAALGL 585 516 LEKCCKAQDQEVCFTEEGGKKLASKTRDALGV 605	SECULT 11 BX56 CBEK56 CBEK56 CBEK56 COBRTS6 COBRTS6	16 EENFKALULIAFAQYLQQCPFEDHVKLVMEYTEFAKTCVADESAENCDKSLHTLPGDKLC 75
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DD 337 DPEVCKREKEEGDAFMGRELCDYAKIHPEHSAELNLRIASGLEKAYKTCCAGEAHNECIA 396 372 KVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLG 431 397 KEEFTLRHEIASAKIKTTGALEKLGPYHFONIMIVRYTGILPRSSDAFLLYITKTLT 456 432 KVGSKCCKHFEARRPCAEDYLSVVLNQLCHEKTRY-SONTKCCTESLVRRPCFSA 490 432 KVGSKCCKHFEARRPCAEDYLSVVLNQLCHEKTRY-SONTKCCTESLVRRPCFSA 490 457 NIGQKCCKLPEDQQMPCSEGGLGMVFAGIC-QNQKTPPENEKLAHCKKDSLAFTPCFAA 515 457 NIGQKCCKLPEDQQMPCSEGGLGMVFAGIC-QNQKTPPENEKLAHCKKDSLKAVNDD 550 411-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	Oy 551 FAAFVEKCCKADDKETCFAEEGKKLVAA 578	Query Match Best Local Similarity 35.7%; Pred. No. 1e-76; DB 11; Length 605; Matches 204; Conservative 100; Mismatches 241; Indels 6; Gaps 3; 16 EENFKALVLIAFAQYLQCOPFEDHVKLVNEVTEFAKTCVADESAENODKSLHTLFODKLC 75;

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Rana shqiperica
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495 ETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMODFAAF 554
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
A/B over-sized serum albumin (Fragment).
Sphenodon punctatus (Harteria) (Tutatral)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
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Local Similarity 47.7%; Pred. No. 5.1e-74;
es 186; Conservative 80; Mismatches 124; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metcalf V.C., Brennan S.C., George P.M., Chambers G.K.; "Partial mRNA sequence for tudtara A/B serum albumin."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF375973; AAW46106.1; Interpro; IRR000564; Serum albumin. Proporty: IRR000564; Serum albumin. Proporty: PR00973; transport prot; 2. PRINTS; PR00973; transport prot; 2. PRNTS; PR00973; transport albumin; 1. SMART; SMO013; Albumin; 2. PROSITE; PS00212; ALBUMIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AA; 45715 MW; 8DE20609657CF753 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SECUENCE FROM N.A.

Metcalf V.J., Brenn
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QBJIA7;
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9.1 DIVCKEEDIDQLYPWTTECCGKAEAERTKCFYEHRE-----VRVEBYKIPNIEESCK 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 AADFVESKOVCKNYAEAKDVFLGMFLYEYARRHPOYSVVLLLRLAKTYETTLEKCCAAAD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 LKEYYEDEHVCENYQKDKRKYLAHFTHDYSRSHQESSPQSCLRVSRGFEMLLEKCCASAN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLK 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCFTKLGPYANYEAPVWDESKLHFTADMCKGSADDQLKTKLVLLVEFLKMKPTCGKEKLT 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 RDEGKASSAKÇRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 KKLINYLEDKHKQKCRVLKEFPERVSQALILVQVSQRFGNAKYDDVBKVITEIAHLNEDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 LTGRMAKIGVYCCGLPDNKKOPCAEEKLDILLGBMCBREKKTFINDNVHHCCVDSYANRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 KDLGBENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKLCTVATLRSTYGEMADCCAKQEPERNBCFLQHKDDNPNLPRLVR-----PEVDVMCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AFHONEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLFKLDEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHECYAKVFDEFKPLVEEPQNLIKQNCBLFEQLGEYKFQNALLVRYTKKVPQVSTPTLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Bushat; TISSUE=Liver;
SIZA11 T. Hotz H.;
"Albumin cDNA sequence of Rana shqiperica: evolutionary changes in frog abbumins.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                                                                Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603 AA; 69293 MW; 340D3723FA010C99 CRC64;
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Ampilbia, Batrachia, Anura, Neobatrachia, Rancidea,
NCBI_TaxID=44326;
                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 30.8%; Score 955; DB 13; Cocal Similarity 33.6%; Pred. No. 9.9e-67; es 190; Conservative 119; Mismatches 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
SERUM ALBUMIN.
     603
                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000264; Serum_albumin.
Pfam; PF00273; transport_prot; 3.
PRUNTS; PR00802; SERUMALBUMIN.
PRODOM; PD0002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
                                               01-MAY-1999 (TrEMBLrel. 10, Created
01-MAY-1999 (TrEMBLrel. 10, Last se
01-UN-2002 (TrEMBLrel. 21, Last an
Serum albumin precursor (Fragment).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U40452; AAD09358.1; -. HSSP; P02768; 1E7B.
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PRELIMINARY;
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603
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232 SKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIA 291
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                                              404 VFKLYITKINEVVKSNCDSYKELGDYFFTNEFLVKYSRAMPQAPTSFLIELTEKVGKVAE 463
                                                                                                                                KCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDE 495
                                                                                                                                                                           TYVPKEFNAETFTFHADICTLSEKERGIKKQTALVELVKHKPKATKEQLKAVMDDFAAFV 555
                                                                                                                                                                                                                                                                                                                                     524 SFVPPTFNPKTMDNPEKLCSTSEDTVQKSKKGLLSELVKSKPNISEEELAATILTFREIQ 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
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Hoplodactylus maculatus.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Gekkota, Gekkonidae;

Hoplodactylus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Metcalf V.J., Brennan S.C., George P.M., Chambers G.K.;
"Partial mRNA sequence for New Zealand gecko albumin.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF375972, AAM46105.1;
InterPro; IPR000264; Serum_albumin.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMITS: PRO0273; transport prot; 2. PRINTS: PR00802; SENUMA.BUMIN. PRODOM; P002486; Serum albumin; 1. SWART; SW00103; ALBUMIN; 2. PROSITE; PS00212; ALBUMIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                             EKCCKADDKETCFAEEGKKLV 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 KLCCEAENKKECFDKKGQEMV 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.04
Matches 173; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
MEDLINE=96145734; PubMed=8561913;
Wang X., Hansen H., Havsteen B.;
"Evidence of the coevolution of snake toxin and its enogenous antitoxin. Cloning, sequence and expression of a serum albumin CENA the chinese cobra.";
                                                                                                                                                                                                                                                                 031134;
031134;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-5701-2022 (TrEMBLrel. 21, Last annotation update)
Cobra serum albumin.
Naja naja (Indian cobra).
Naja naja (Indian cobra).
Naja naja (Indian cobra).
Enpaidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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                                                                                                                                                                                                                                               614 AA
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       AVMDDFAAFVEKCCKADDKETCFAEE 571
                                              |::| |::|| |::|| |::
567 EVIESFRKTVVECCAAENQQACFDEK 592
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PRINTS; PR00802; SRNMALBUMIN.
Probom; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 2.
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ઠે qq Search completed: October 27, 2003, 15:21:05 Job time : 108 secs